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419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 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; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 602/99,584
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 602/99,584
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US 10-175 042 17

Query Match
Best Local Similarity 31.4%; Score 2376.5; DB 12; Length 1498;
Matches 534; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

QY 122 MGGTALMAWYKGRFLVVELLSHQANSTVJGQYVYPIWAAAGRHATVHLLQNG 161
DB 1 MGGTALMAWYKGRFLVVELLSHQANSTVJGQYVYPIWAAAGRHATVHLLQNG 59
QY 162 AKVNSCKYGTITLWAKKEHE VKHLLAKARNUCJANSMTALVAVKGGYTGVP 221
DB 60 AKVNSCKYGTITP WAAARKEHEVKHLLAKARNUCJANSMTALVAVKGGYTGVP 119
QY 222 EILKRNPNVLTKKGNATVIAASKEGHEIVQLLDGACTVYNIIPDRSGDTVLCGAVGGHVEIVRAJLQKQVADIDR 299
DB 20 EILKRNPNVLTKKGNATVIAASKEGHEIVQLLDGACTVYNIIPDRSGDTVLCGAVGGHVEIVRAJLQKQVADIDR 179
QY 292 HVEIVRAJLQKQVADIDRQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 359
DB 190 HVEIVRAJLQKQVADIDRQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 381
QY 342 KATKRNIEVWELLQKQVADIDRQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 419
DB 240 KATKRNIEVWELLQKQVADIDRQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 441
QY 402 NKAGETPYNIDSHOKSIITQIFGARHLSPTEITGEMLGVDLYSSALADILSEPTMOPPICVGLVAONGSGKSFLLKK 479
DB 300 NKAGETPYNIDSHOKSIITQIFGARHLSPTEITGEMLGVDLYSSALADILSEPTMOPPICVGLVAONGSGKSFLLKK 501
QY 462 CVGLVAONGSGKSFLLKKQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 538
DB 360 CVGLVAONGSGKSFLLKKQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 561
QY 520 DTRNAIAISGKSFLLKKQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 598
DB 420 HFNLGAVNSKSFLLKKQENKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 618
QY 582 NPPELPECTTKALPVRFLEFTEGNSASVTEINGAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 656
DB 480 NPPELPECTTKALPVRFLEFTEGNSASVTEINGAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 677
QY 642 RTEESQKKKK 653
DB 540 RTEESQKKKK 551

RESPOST 13
US-10-021-571-8
; Sequence 8, Application US/10021-571
; Publication No. US20030166036A;
; GENERAL INFORMATION:
; APPLICANT: CHAO, Moses V.
; INVENTOR: KONG, Haeyoung
; TITLE OF INVENTION: A TRANSMEMBRANE PROTEIN AS A DOWNSTREAM TARGET OF NEUROTROPHIN AND
; TITLE OF INVENTION: RECEPTOR TYROSINE KINASES, DNA ENCODING SAME AND MONOCLONAL ANTI
; FILE REFERENCE: CHAO11A
; CURRENT APPLICATION NUMBER: US/10/021-571
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,909
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Drosophila
US-10-021-571-8

Query Match
Best Local Similarity 37.6%; Score 2376.5; DB 12; Length 1498;
Matches 552; Conservative 272; Mismatches 577; Indels 117; Gaps 36;

QY 1 MSVVSQGVVNYVEEENIPALKE-KKQVDEHNECCGOTPLMLAAEQGVNEIVKELK 59
DB 23 MGSQGHFALLCYIDNDISGRAILDSRHUTIDRDENAVITLVMVAGRGUTAFVREFLA 82
QY 60 NGANCNLEDCJNMTALVIAASKEGHEIVVEELLKSGASLEHDMGGTALMAWYKGRITDV 119
DB 83 RGADVQVEDJNMTALVIAASKEGHEIVVEELLKSGASLEHDMGGTALMAWYKGRITDV 142
QY 120 VELLKSGASLEHDMGGTALMAWYKGRITDVIAAAGRHADIVHLLQNGAKVNSCKYGTITP 179
DB 143 VRLLKSGASLEHDMGGTALMAWYKGRITDVIAAAGRHADIVHLLQNGAKVNSCKYGTITP 201
QY 160 RKHLEQVNEHLLANGADVDOEGANSMTALVAVKGGYTGVPVAVKGGYTGVPVAVKGGYTGVP 239
DB 202 ERGNVEVOTLLKAGANVDTAGVYVMTPLVAAAGSGHTDCVSSILEKKNPNVNAALQKGMT 261
QY 240 ALMIASKEGHEIVVQDLDGACTVYNIIPDRSGDTVLCGAVGGHVEIVRAJLQKQVADIDR 299
DB 262 ALMIASKEGHEIVVQDLDGACTVYNIIPDRSGDTVLCGAVGGHVEIVRAJLQKQVADIDR 321
QY 300 QDNRKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 359
DB 322 QDNRKTAIAWAKNATNRDILQCPOTEITKQGETPLIKATKRNIEVWELLQK 381
QY 360 AKVNSCKYGTITP WAAARKEHEVKHLLAKARNUCJANSMTALVAVKGGYTGVP 419
DB 382 AKVNSCKYGTITP WAAARKEHEVKHLLAKARNUCJANSMTALVAVKGGYTGVP 441
QY 420 LTQIFGARHLSPTEITGEMLGVDLYSSALADILSEPTMOPPICVGLVAONGSGKSFLLKK 479
DB 442 LGQVFGARRLNTDSEGMUGYELLYSSALADILSEPTMOPPICVGLVAONGSGKSFLLKK 501
QY 480 EDEMKFAGQUTEPPLFQFSGKQVVELTLLQGGGLVFAFPV-DTNLAIAISLSPALITY 538
DB 500 EDEMKFAGQUTEPPLFQFSGKQVVELTLLQGGGLVFAFPV-DTNLAIAISLSPALITY 561
QY 520 EDEMKFAGQUTEPPLFQFSGKQVVELTLLQGGGLVFAFPV-DTNLAIAISLSPALITY 598
DB 562 EDEMKFAGQUTEPPLFQFSGKQVVELTLLQGGGLVFAFPV-DTNLAIAISLSPALITY 618
QY 599 LFTDYNR-SSVGGETSIAEMIATLSDACEREFGLATRLFEVFE-ESQKKKKKTC 656
DB 619 HFAEANSASPT-GDGAVALMLAALDDAIESHYGLATRLYBAFRPKCLKVDVGARWRMC 677
QY 657 CLPSEVIFEFIVGCIAGITLLAIF-----RVDFKGLTVNAILISIASVWGLAFVLCRT 711
DB 678 CLPSEVIFEFIVGCIAGITLLAIF-----RVDFKGLTVNAILISIASVWGLAFVLCRT 735
QY 712 WQVLDLSLNSCRKRIHSAASKLHKJKEGPMKVKCEVELMARMKTI-DSFTQNTQLV 771
DB 736 LAKVFSLSFTSHIRVLKRAV-----RSSSESAPLTMILGAEVAVMTDMVKCLDAFTNQOSRLV 791
QY 772 VIIDGLDACEQDKVLOWJTVRVLPF--KGFIAIFASDPHIITKAINONLSVLRSNT 829
DB 792 GVIDALDSCDTERITLLNVAQTLLSSNRPFLVLLISVDPHVIAKAAEAKSRRRTFEGGI 851
QY 830 NGRDYMRIIVHLPVFLNSRGLSNARKFLVTS-----ATNGDITCSD--TTCTQEDTDRV 882
DB 852 GGRDFELNIVHLPVYVLSNGSKRKVQRAQK-ALLFKRSGGQYQDDGPTLG-HSVSARRL 910
QY 883 SONS--LGEHTKL-----GSKTALNR-----RDTYRRRQMQRTITRMSFDLTKL 925

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DB 1441 SERSEFQTLKLGSLRYQKAPSEDESDGKESLNTPLDKKKLRKAKGVKVEVPKS 1499

QY 1501 QHSAPRTTF:KAKYKLSALLQKSSDSYVSHSESPHSHKAEAAZQSLKANI 1560

DB 1500 PHSAPRTTF:KAKYKLSALLQKSSDSYVSHSESPHSHKAEAAZQSLKANI 1559

QY 1561 ELEDEHSGREGVPHSLHJGQDILARMALQREKSPSEGLIASSPESHPAQQAFV 1620

DB 1560 ELEDDHSGREGVPHSLHJGQDILARMALQREKSPSEGLIASSPESHPAQQAFV 1619

QY 1621 LNPSTSTVTLNNTATPTNANQVHLEHLPETSOVLESPGSPFATUNENLAKNAK 1680

DB 1620 LNPSTSTVTLNNTATPTNANQVHLEHLPETSOVLESPGSPFATUNENLAKNAK 1679

QY 1681 RSORSSYTRLSKASELH AASSESQFGDERESID 1715

DB 1680 RSORSSYTRLSKQPPHHAASSESQFGDERESID 1715

RESULT 5

AAV19025

ID AAM19025 standard; Protein; 1715 AA.

AC AAM19025;

XX 22-NOV-2001 (first entry;

XX Human; polypeptide SEQ ID NO 2100.

XX Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer;

KW peripheral nervous system; neurogathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy Drager Syndrome; Chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukemia.

XX Homo sapiens.

XX NC20015312-A1.

XX 26 JUL 2001.

XX 26 DEC 2000; 2000MO-US34241.

XX 21-JAN 2003; 2000US 048471.

XX 25-APR-2003; 2000US 056131.

XX 02-JUL-2003; 2000US 056041.

XX 19-JUL-2003; 2000US 057111.

XX 01-AUG-2003; 2000US 065451.

XX 14-SEP-2000; 2000US 066291.

XX 19-OCT-2000; 2000US 069103.

XX 29-NOV-2000; 2000US-0727344.

XX HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian X, Ren F, Wang C;

PI Wang J, Wang Z, Wehrman T, Xu C, Xie M, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Oranac R.

XX WU: 2001-442253/47.

DB N 5589; AA1581A1.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries

XX Example 4; SEQ ID NO 2170; 10074pp; En3:180.

XX The invention relates to human nucleic acids (AA157758-AA161365) and

CC the encoded polypeptides (AAV35542-AA44221) with nootropic,

CC immunosuppressant and cyostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 1715 AA.

Query Match 93.4%, Score 8266, DB 22; Length 1715;

Best Local Similarity 92.7%, Pred. No. 0;

Matches 1591; Conservative 53; Mismatches 70; Indels 2; Gaps 2;

QY 1 XSVLIISQSTHYVBEENIPALKALLEKCKYVDNECCQTPIMJAAAGQNVVEIKELKN 60

DB 1 XSVLIISQSVHYVBEENIPALKALLEKCKYVDNECCQTPIMJAAAGQNVVEIKELKN 60

QY 61 GANCKLEFQKWTALISASKGSHIYVEELKSGASLEHDMGGTALMWACYGRTDVV 120

DB 61 GANCKLEFQKWTALISASKGSHIYVEELKSGASLEHDMGGTALMWACYGRTDVV 120

QY 121 ELLSHDAPSVTIGIQSVYPIIWAAGRGHADI VELLQNGAKVNCSDKYGTPPLWAAAR 180

DB 121 ELLSHDAPSVTIGIQSVYPIIWAAGRGHADI VELLQNGAKVNCSDKYGTPPLWAAAR 180

QY 181 KHLCEVPHLLAKXADVPCRGANSATLIVAKGYTOSVKEILKRNPNVNTDKDHTA 240

DB 181 KHLCEVPHLLAKXADVPCRGANSATLIVAKGYTOSVKEILKRNPNVNTDKDHTA 240

QY 241 LMIASKEGHEHIVCOLLDAGTYVNIIPDSGPTVILGAVRGHVEIVRALLQKAYADIDRG 300

DB 241 LMIASKEGHEHIVCOLLDAGTYVNIIPDSGPTVILGAVRGHVEIVRALLQKAYADIDRG 300

QY 301 QNKTAJYWAYVEKGNATVVRDILQCNPDTEICTKDGTEPLIKATKMRNIEVVELLDKGA 360

DB 301 QNKTAJYWAYVEKGNATVVRDILQCNPDTEICTKDGTEPLIKATKMRNIEVVELLDKGA 360

QY 361 KVSAYVKKEDTPLHVAISGRSRRJAEILLRNPKGRLYRNKAGETPNYDCSHOKSIL 420

DB 361 KVSAYVKKEDTPLHVAISGRSRRJAEILLRNPKGRLYRNKAGETPNYDCSHOKSIL 420

QY 421 TQIFGAPHHPTETDGLMGLYDLYSSALATLSEPTMQPFCVGYACGSKSEFLKKL 480

DB 421 TQIFGAPHHPTETDGLMGLYDLYSSALATLSEPTMQPFCVGYACGSKSEFLKKL 480

QY 481 EDEKTFPAGQTEELFQFSWLIIVETLLCCGLSLVFAFPVDTNLAIASISFLALYIF 540

DB 481 EDEKTFPAGQTEELFQFSWLIIVETLLCCGLSLVFAFPVDTNLAIASISFLALYIF 540

QY 541 FIVIFYGGRSESNWAKALSTRARHIGVLEILLFKLMFVNPPELPEOTTKALPVRLF 600

DB 541 FIVIFYGGRSESNWAKALSTRARHIGVLEILLFKLMFVNPPELPEOTTKALPVRLF 600

QY 601 TDYNRLSSVAGETSLSAEMIALTSLDACEREFGLATRLFRVFRTEESQCKKKWKTCCLPS 660

DB 601 TDYNRLSSVAGETSLSAEMIALTSLDACEREFGLATRLFRVFRTEESQCKKKWKTCCLPS 660

QY 661 FVIFELVGGTLAGITLLAIFRVPKHLTVNAIILSIASVVGGLAFVLCNRTMWQVLDLL 720

DB 661 FVIFELVGGTLAGITLLAIFRVPKHLTVNAIILSIASVVGGLAFVLCNRTMWQVLDLL 720

QY 721 NSQRKPLHSAASKLHKLXSEGMKVLKCEVELMARMAKTIDSFTQNTRLVVIIDGLDAC 780

DB 721 NSQRKPLHSAASKLHKLXSEGMKVLKCEVELMARMAKTIDSFTQNTRLVVIIDGLDAC 780

QY 781 EODKVLQKLTIVRVLFSGPIIAFASDPHILIKAINONLSVLPDSNNGHGDYMRNVH 840

DB 781 EODKVLQKLTIVRVLFSGPIIAFASDPHILIKAINONLSVLPDSNNGHGDYMRNVH 840

Query Match	93.4%	Score 8246	DB 24	Length 1715
Best Local Similarity	92.7%	Pred. No. 0		
Matches 1591	Conserved: 53	Mismatches 70	Indels 2	Gaps 2
Query	MSVLISQSNINIVVEEENIPALKAL	EKKQYDERNECCQTPLMLAAEQGNVE	YKELLKKN	60
DB	MSVLISQSNINIVVEEENIPALKAL	EKKQYDERNECCQTPLMLAAEQGNVE	YKELLKKN	60
Query	GANCNLEEDFNMTAL	SASKEGH	IVLELLKSGASLEHDMGWTAL	MACYKGP
DB	GANCNLEEDFNMTAL	SASKEGH	IVLELLKSGASLEHDMGWTAL	MACYKGP
Query	ELLSSHGCAINVTG	QYSVYP	IWAAGRHAD	IVHLLQNGAKYK
DB	ELLSSHGCAINVTG	QYSVYP	IWAAGRHAD	IVHLLQNGAKYK
Query	KGHLECVYVHRA	AMGADVDOEGANSMTA	IVAVKGYTQSVKEI	LKRNPNVNLTKD
DB	KGHLECVYVHRA	AMGADVDOEGANSMTA	IVAVKGYTQSVKEI	LKRNPNVNLTKD
Query	LVYASKEGH	IVVCDL	LAGTVNIPDRSGDTV	IVGAVRGHVEI
DB	LVYASKEGH	IVVCDL	LAGTVNIPDRSGDTV	IVGAVRGHVEI
Query	QDNKTA	YWAVEKGNAT	WYVDILQCNPOTE	CTKDGTEPLIKAT
DB	QDNKTA	YWAVEKGNAT	WYVDILQCNPOTE	CTKDGTEPLIKAT
Query	KVSAVKK	ITP	LVHVAIPDRSPRLAELL	LRPKQRLLYRPNKAGET
DB	KVSAVKK	ITP	LVHVAIPDRSPRLAELL	LRPKQRLLYRPNKAGET
Query	TCVFGAS	IVLETDG	IVGVYLYSSALAD	IVSEVITQFPI
DB	TCVFGAS	IVLETDG	IVGVYLYSSALAD	IVSEVITQFPI
Query	EDSMKTF	AL	TEP	IFQPSKLIVF
DB	EDSMKTF	AL	TEP	IFQPSKLIVF
Query	PIVYFGSP	PESES	WNAVALSTR	IVARHIGY
DB	PIVYFGSP	PESES	WNAVALSTR	IVARHIGY
Query	TCVNR	LVSSW	IVETS	LAEMTATLS
DB	TCVNR	LVSSW	IVETS	LAEMTATLS
Query	FVIFL	FI	IVIIAGIT	LA
DB	FVIFL	FI	IVIIAGIT	LA
Query	NSQPK	B	IVHSAASK	JKH
DB	NSQPK	B	IVHSAASK	JKH
Query	EQQR	LV	IVK	IVL
DB	EQQR	LV	IVK	IVL

DB 327 VSAVKKGGTDLURIA:RGRSBAKAEALLNPNKGRLLVRENKAGETPVNLCDSHOKSILT 396
QY 422 QIFGARHLSPTETCDXLCYCYSSALADILSEPTWCPPIVGLVACWAGSGFALKKLE 461
DB 397 QIFGARHLSPTETCDXLCYCYSSALADILSEPTWCPPIVGLVACWAGSGFALKKLE 446
QY 462 DEMKTFAGQTEPLPQFOSMLVPELILVCELVNWFAPFVEMLALALASLALATVYFF 541
DB 447 DEMKTFAGQTEPLPQFOSMLVPELILVCELVNWFAPFVEMLALALASLALATVYFF 506
QY 542 IVYFGRRGEGSWNNAWAI STGLAPHI HDELFKLYPVSIFERACUTRALPKVLEPT 601
DB 507 IVYFGRRGEGSWNNAWAI STGLAPHIHDELFKLYPVSIFERACUTRALPKVLEPT 566
QY 602 DYNELSSVGRGSLAMIAIATLSDA:EPLEFELATRIERVFVFEKQKKNKWT 656
DB 657 DYNELSSVGRGSLAMIAIATLSDA:EPLEFELATRIERVFVFEKQKKNKWT 620

RESULT 10
AAEC1235
ID AAE01035 standard; Protein: 151 AA.
XX AAEC1035;
XX
DT 64-001-1001 (first entry)
XX
CE Human death domain-containing receptor (DCCR) protein; from HCDX59 clone.
XX
KW Human; death domain-containing receptor (DCCR); immunosuppressive;
KW antiarthritic; antineuritic; antiproliferative; cytostatic;
KW cardiac; vasodilator; cerebroprotective; neurotropic; neuroprotective;
KW antibacterial; virucide; fungicide; opthalmological; gene therapy;
KW immunodeficiency disease; Acquired immune deficiency syndrome;
KW AIDS; leukaemia; autoimmune disease; systemic lupus erythematosus;
KW hyperproliferative disorder; neoplasia; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; cardiovascular disorder;
KW neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW ocular disorder; corneal infection; degenerative disease; SMA; apoptosis;
KW spinal muscular atrophy; epithelial cell proliferation; infection;
KW cancer; wound healing; skin aging; chemotaxis; HCDX59 clone.
XX
OS Homo sapiens.
XX
PH location/chain: 110-116
FT 396-416
FT /label= Transmembrane domain
FT Domain
FT 426-446
FT /label= Transmembrane domain
FT Region
FT 64-69
FT /label= Immunogenic epitope
FT Region
FT 131-136
FT /label= Immunogenic epitope
FT Region
FT 164-169
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FT 197-203
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FT /label= Immunogenic epitope
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XX WO200129663-A2.
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XX 24 APR 2001.

XX 17-OCT 2003: 200TWO US28666.
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PR 18 OCT-1999: 99US 0159565.
PR 24 NOV-1999: 99US 0167246.
XX
XX (HUMAN): HUMAN DEATH DOMAIN SCT INC.
XX N: J. Ruben SV;
XX
XX WPI: 2001-10616-1
XX N-PSDB: AAD04716
XX
PT New death domain-containing receptor polynucleotides and polypeptides,
PT useful for treating and diagnosing cancer.
XX
XX Claim 1: Page 292-294; 298pp: English.
XX
CC The patent discloses novel death domain-containing receptor (DCCR)
CC cDNAs and their corresponding proteins. DCCR cDNA and protein are
CC used to prevent, treat or ameliorate a medical condition in mammals.
CC They are also used in diagnosing a pathological condition or
CC susceptibility to a pathological condition. The DCCR protein and
CC its antibodies are used in the diagnosis and treatment of disorders
CC such as immunodeficiency diseases (e.g. Acquired immune deficiency
CC syndrome (AIDS), leukaemia) autoimmune diseases (e.g. systemic lupus
CC erythematosus, rheumatoid arthritis), hyperproliferative disorders
CC (e.g. neoplasms of the breast or liver), cerebrovascular disorders
CC (e.g. cerebral ischaemia, angiogenesis), cardiovascular disorders
CC (e.g. cardiac arrest), neurodegenerative diseases (e.g. Alzheimer's
CC disease, Parkinson's disease), ocular disorders (e.g. corneal
CC infection), degenerative diseases (e.g. spinal muscular atrophy-SMA),
CC cancer, aberrant apoptosis, disorders of the placenta or uterus and
CC infections caused by bacteria, viruses and fungi. The DCCR proteins
CC are used to aid wound healing and epithelial cell proliferation.
CC to prevent skin aging due to sunburn, to maintain organs before
CC transplantation, to support cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The DCCR sequences are used
CC in correcting aberrant cellular apoptosis by gene therapy.
CC The present sequence is human death domain-containing receptor
CC (DCCR). Protein from clone HCDX59.
XX
SQ Sequence 551 AA.
Query Match 31.4%; Score 2762.5; DB 22; Length 551;
Rescaled Similarity 96.7%; E-Value 2.1e-210;
Matching 534; Conservative 8; Mismatches 9; Indels 1; Gaps 1;
QY 162 KGGWTAIMKAA YKGETVVELLSHGANSVVTG:QYVYPIIWAAGRGHAD:VHLLQNG 161
DB 1 KGGWTAIMKAA YKGETVVELLSHGANSVVTG: YSVYPIIWAAGRGHAD:VHLLQNG 59
QY 162 AKVNSKRYGTTPLVWAARKGHLECVKHLJANGADVDOEGANSMTALIVAKGGYTSVK 221
DB 60 AKVNSKRYGTTPLVWAARKGHLECVKHLJANGADVDOEGANSMTALIVAKGGYTSVK 119
QY 222 ELTKENNVNLTGKGNLTALMIASKEGHE:VVCULLDAGTYVNI:PDGSDTVLIGAVRG 281
DB 120 ELTKENPNVLTGKGNLTALMIASKEGHE:VVCULLDAGTYVNI:PDGSDTVLIGAVRG 179
QY 282 HVEIVRALQKYADIDIRGQDNKTALYWAVEKGNATWVRDILQCNPDTEICTKGETPLI 341
DB 180 HVEIVRALQKYADIDIRGQDNKTALYWAVEKGNATWVRDILQCNPDTEICTKGETPLI 239
QY 342 KATQRNIEVELLDKAKVSAVDKGGTPLHVAIIRGSRRLAELLRNPKDGLLYRP 401
DB 240 KATQRNIEVELLDKAKVSAVDKGGTPLHVAIIRGSRRLAELLRNPKDGLLYRP 299
QY 402 NKAGETPVNIDCSHOKSILTOIFGARHLSPTETDGMGLGYDLYSSALADILSEPTWQPI 461
DB 300 NKAGETPVNIDCSHOKSILTOIFGARHLSPTETDGMGLGYDLYSSALADILSEPTWQPI 359
QY 462 CVGLVACWAGSGFALKKLEDEMKTFAQQTEPLPQFOSMLVPELILVCELVNWFAPFV 521


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154 CGHRYVAHLINVTGKGVKRALFIAAPNDVTRTAAVLLLELPFVSKIGETILHIA 213
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RESULT 5

AB2149
 hypothetical protein, A12748 (imported) : Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. strain PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of *Arabaena* sp. strain PCC 7120
 C:Date: 14-Dec-2001
 C:Accession: AB2149
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguc
 Nakazaki, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
 DNA Res. 9, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A
 A:Reference number: A1207; NCBI:2159285; PMID:11759840
 A:Accession: AB2149
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1426 aa
 A:Cross-references: GABAC0019; PIDN:DAB74447.1; PID:G17131841; GSPDB:GNC0179
 A:Experimental source: strain PCC 7120
 A:Genetics:
 A:Gene: A12748

Query Match 4.3% Score 55% Lh 21 Length 4261


```

DB 326 MGRSRH... GURVLP... PRCARPTTICELQ... 354
CY 783 DKVLQMDTVRVVPSKGPFIATFA...PHILIKALNQNSWSEISVIN...INHL RH...
DB 955...KPKCKSTPRPL... --AAREELASGFIATPTI...ELSPVIVE... 993
CY 842 PVPL...NRGLSNAPKPLVYVATNG...SNTTTCGDTI...P...K...S...K...N... 500
DB 994 PHFASHUG...VRELVYVSENV... --WREHP...K...Q...N... 1041
CY 901 RROTYRRKQCPITROYS...P... --W...S...P...M...T...P...K...N... 957
DB 1042 SLEFLKRRVRC... TR...V...V...V...V...V... 1042
CY 959 QITNWRRLASKNITQWYFTSW... --L...E...E...K...P... -- -- -- -- 1005
DB 1092 QATPENAVTKVLAIQ... -- -- -- -- -- -- -- -- -- -- 1137
CY 1004 ISK... -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1042
DB 1138 RRPFRPIG...PLPPSWT...N...P...S...S...V...S...Q...A...V... 1197
CY 1243 RCVVTEPLCTVNLGK...PELLADV...A...P...Q...N... -- -- -- -- -- -- 1202
DB 1194 NECAP... -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1242
CY 1173 CSSASFUPPGVUSVQTHSYV... -- -- -- -- -- -- -- -- -- -- -- 1152
DB 1243 VIFAMNDPBG... -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1269
CY 1163 LRC...E...L...D...N...M...K...Y...C...T...I...K... -- -- -- -- -- 1216
DB 1220 LQHNFEV...V...K...S...D...I...E...V...L...N...S...I...P...A...L... 1323
CY 1217 VLEKPSYSSQVF... -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1298
DB 1304 AMPKVRGSSNF...S...L...S...E...I...K...A...V... -- -- -- -- -- 1383
CY 1259 L... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1314
DB 1384 LKYSLSSESTPSLSGTEQAKMKVAVIA... -- -- -- -- -- -- -- -- -- 1433
CY 1415 ELSKTHKVCAYRCAVREYLAQ... -- -- -- -- -- -- -- -- -- -- -- 1472
DB 1414... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1468
CY 1371 ST... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1426
DB 1469 TAC... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1443
CY 1426... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1449
DB 1524 PASLICALSSP...PACQVNF...V...A...L...P...A...T...H...T...W...E...M...V...W...A...L...T... 1562
CY 1469 ESATGRVQITPKSKMIR...K...A...L...P...E... -- -- -- -- -- -- -- -- 1529
DB 1581 SS... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1631
CY 1529 S... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1580
DB 1632 NGLICLLEQEGQRSEELPKPKK... -- -- -- -- -- -- -- -- -- -- -- 1686
CY 1581 QCPILARMSICSEK... -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1641
DB 1687... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1701

```

RESULT 7

A35049
 N: erythrocyte splice form 2, hu-
 N: Alternate names: ankyrin 2.2, erythrocyte, ankyrin 8
 N: Contains: ankyrin 2.2, erythrocyte
 C: Species: Homo sapiens (man)

C: Date: 27-Jul-1992 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
 C: Accession: A35049
 R: Lamber, S.; Yu, H.; Pichal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A: Title: cDNA sequence for human erythrocyte ankyrin.
 A: Reference numbers: A35049, M101901761.0, PMID:169849
 A: Accession: A35049
 A: Status: Preliminary
 A: Molecule type: mRNA
 A: Residues: 11880 (aa)
 A: Cross-references: JF: M: 4880
 C: Genes: ANK
 A: Gene: GDB:ANK, ANK
 A: Cross references: GDB: 118739, OMIM:182920
 A: Map Position: 8p11.2-8p11.2
 C: Superfamily: ankyrin; ankyrin repeat homology
 C: Keywords: alternative splicing; cytoskeleton
 F: 2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F: 2-1513/1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F: 44-76/Domain: ankyrin repeat homology <AN01>
 F: 77-109/Domain: ankyrin repeat homology <AN02>
 F: 110-142/Domain: ankyrin repeat homology <AN03>
 F: 143-171/Domain: ankyrin repeat homology <AN04>
 F: 172-204/Domain: ankyrin repeat homology <AN05>
 F: 205-237/Domain: ankyrin repeat homology <AN06>
 F: 238-270/Domain: ankyrin repeat homology <AN07>
 F: 271-303/Domain: ankyrin repeat homology <AN08>
 F: 304-336/Domain: ankyrin repeat homology <AN09>
 F: 337-369/Domain: ankyrin repeat homology <AN10>
 F: 370-402/Domain: ankyrin repeat homology <AN11>
 F: 403-435/Domain: ankyrin repeat homology <AN12>
 F: 436-468/Domain: ankyrin repeat homology <AN13>
 F: 469-501/Domain: ankyrin repeat homology <AN14>
 F: 502-534/Domain: ankyrin repeat homology <AN15>
 F: 535-567/Domain: ankyrin repeat homology <AN16>
 F: 568-600/Domain: ankyrin repeat homology <AN17>
 F: 601-633/Domain: ankyrin repeat homology <AN18>
 F: 634-666/Domain: ankyrin repeat homology <AN19>
 F: 667-699/Domain: ankyrin repeat homology <AN20>
 F: 700-732/Domain: ankyrin repeat homology <AN21>
 F: 733-765/Domain: ankyrin repeat homology <AN22>
 F: 766-798/Domain: ankyrin repeat homology <AN23>

Query March 6, 2003 Score 553 DB 2, Length 1880

Best local similarity 20.5% Pied No 5, 40-24

Matches 388, Complement 287, Mismatches 648, Indels 579, Gaps 73

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CY 81 EKAL... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 90
DB 94 VRL... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 153
CY 91 EGH... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 81
DB 154 QGH... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 213
CY 94... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 138
DB 214 AHY... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 272
CY 139 VY... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 198
DB 273 LTP... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 332
CY 199... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 225
DB 333 DT... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 392
CY 226 RRP... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 285
DB 393 TGA... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 452
CY 286 VRA... -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 345

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Db 453 AYLLGQNKAKKAKAKDDQTPLEKAPRI HIRNVAKALLNNANPKUATIAHTPULHIAZ 512
QY 346 MRNIEVEILLDKAKUSAVQKQATPC HVATPJRSPRIAEILLANPKRIKLVYENKAS 405
Db 513 EGHVEVYVALLKEASCAWTKKGTPLHVAAY HVVPSAEILE RLA HPSAAI 566
QY 406 E TPYNIDONIC -- KALID -- -- -- -- -- -- -- -- -- -- -- -- -- 427
Db 567 KNULEPLHVAHINHLINIVKILPS LRIHSDPAWVYTHIAPKQVQVPSLLQYAG 626
QY 428 -- 462
Db 627 SANVAAGVATVHLAAQZCHREVAALD QKAM INHDSFQI THHVAHBNHVAW 686
QY 463 -- 501
Db 687 LIKRTWVATKXVTPHVAHINHLINIVKILPS LRIHSDPAWVYTHIAPKQVQVPSLLQYAG 626
QY 502 -- 543
Db 745 GHTDIVTLLKNG -- ASPKNSGDTTALAKRLWISWTVLKV7 -- -- -- -- -- 789
QY 554 SKNNWALSTRLAHGYHLLKPKYVHNPBLSGOTFALLVRFPTVYVCLSGUG 612
Db 790 TDTSEVVSDFIR NSFTPTVDLIDHDEGEENIS -- -- -- -- -- -- -- -- -- 840
QY 613 TSAEMIALTSKATEREERGFATIRER -- -- -- -- -- -- -- -- -- -- -- 662
Db 841 KELLDFVPLGVVR -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 892
QY 663 TELEVOCTIATILATFVVDHNTTHALL TASVYVAFVATVQVWVWVLS LIA 722
Db 893 -- 925
QY 723 CSESLHSAASKHKLKSKGKXKLP EULIMAPKATILSFTLNTJRAVYHIDHAG 782
Db 926 MROSHRN -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 954
QY 783 DKVYLOTVRVLESKSPATFAPATHTLIPALKNQWVPIHNSHNYEN IVR 941
Db 955 -- 993
QY 843 PVPL NSRGSNAKKPLVTSAINR TLEHDTTJGQHTPRVYNGVYVPLVSGTAN 900
Db 994 PEPASHRG -- ESRVWLSNGLA -- -- -- -- -- -- -- -- -- -- -- -- -- 1041
QY 901 RENTYBRQWCTIPQWVSTVETV -- -- -- -- -- -- -- -- -- -- -- -- 957
Db 1042 SLEHIEEPVYRIT -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1090
QY 958 QTFPLMRASWINDKRLNITVSLVSLVLA TLEHDTTJGQHTPRVYNGVYVPLVSGTAN 900
Db 1092 QATFENAVTKVSKALL -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1137
QY 1006 ISK -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1042
Db 1138 RRKHSRPIGLRPLPSTWTPSPHSLVPTSTLSTVSLVSLVLA TLEHDTTJGQHTPRVYNGVYVPLVSGTAN 900
QY 1043 RYKVTFLPCTVLEPRNREIAPVAPASLQNTSLAVYHIDHAG 782
Db 1198 NCCANF -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1242
QY 1103 CSHASRSPRGVVSQCPHVSYSVLS HQHFFPFAAGLA -- -- -- -- -- -- -- 1162
Db 1243 VIFAKMNDPREG -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1269
QY 1263 LRQLEGQKQMPVYCTTIR -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1316
Db 1270 LECHENVEVARASDIEVLENSLAEK45 -- -- -- -- -- -- -- -- -- -- -- 1323
QY 1277 VLENVSQVVP -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1298
Db 1324 AMPVVEVROSSREPNSSLEKZAVFVCHILHLNITVPIKAKSGANREPTITFA 1393

QY 1259 L--TELSSQTYTLNLFPE-ELNTLGLDEGAPRHSNLSWOSQTRTP-SJSSLSNQSSSI 1314
Db 1384 LRVSLSEFNTLSLSGTECAEMKQAVISE---HLG-SWAEARELOFSVEDIN--- 1433
QY 1315 HSKLTKVQVAYDCAVREYIAQNSULEGGTSGSTISGRSPHSYTYI--QCSSSGGSIH 1372
Db 1434 -----KIVKENTPNSLLEQSVALLNL--- -- -- -- -- -- -- -- -- -- 1466
QY 1473 STDFQ HRAKPEJELKQEDGRKSFNKK--EGDVYSSSGVSTNEASPIQDTTEDE--- 1425
Db 1469 TALLSILKALREYVNI EUSJQKSRNKLKURPHFTDZYSLSPSQMGYSLSL-----CQELLS 1523
QY 1426 KINQOSKIL-----IPGXSSRPSLFOFDLKKGCGHYQKLPSEHED 1468
Db 1534 PASLQKALSNILKALQYWNVAILLDAPLAATEHTMLEMSDMQVWSAGLT-PSLVTAE 1582
QY 1469 ESGTQVQVTHICSXKIFTKRLKAKQRECAPSPOHSAPERTIFIKAKKEYLSDALDKKDS 1528
Db 1583 SS---LECK--AEDSCATHEWKLEGAJSEEPGFELGSLVELVEDTVERDAT 1631
QY 1529 S -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 1580
Db 1632 NGLIDLECHLQCSERKLPGSKKQDDATGAGQ LSENEVSVSHQRCQARITHS -- 1686
QY 1581 CPTTAKMTLSRDK-----KSPRCSHLSASSPESW 1612
Db 1687 PTVGVTMSQRLQCDWADGSIYSVQLDAAQSSW 1721

RESULT 8
T42716
Ankyrin 3, splice form 4 : mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jan-2000 sequence_revision 11 Jan-2000 text_change 04-Mar-2000
C:Accession: T42716
P:Access: EMBL, GenBank, KJ, L, F.M., Eicher, E.M., Higgins, A., Yialamas, K., Turtzo, J., Cell Bio. 130, 311-330, 1995
A:Title: Anky repeat domain (ankyrin), a widely distributed new member of the ankyrin gene repeat domain.
A:Reference number: 222137, MJD:95145633, PMID:7615634
A:Accession: T42716
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: cDNA
A:Residues: 1361 (85%)
A:Accession: 222137, MJD:95145633, PMID:7615634
A:Experimental source: strain C57BL/6J; kidney
C:Keywords: alternative splicing
Query Match 6.2%; Score 552; DP 2; Length 1961;
Best Local Similarity 29.12%; Fwd. No. 6.7e 24;
Matches 427; Conservative 289; Mismatches 674; Indels 724; Gaps 85;
C:Keywords: alternative splicing

QY 14 EENTFACFALFELKQVWERNECQTPHMLAAGQVAVIKELKNGANKLESLDKNT 73
Db 66 KCHVETVSHLQRPANVDAATKKENTALHSLAQAEVVKLVTVNGANVAGSQNSFT 125
QY 74 ALISAKSKSHHIVVELLKSGSLSHRDMGWTALMMACYKGRDVBELL----- 124
Db 126 PLVMAAGJENHLEVRFLDNGASQSLATEDGFTPLVALQQCHQVWSLLENDTKGVR 185
QY 125 -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- -- 135
Db 186 PALHNAKPTDTRAAALLQNDTNACVSKSGFTPLHIAAHYKINVTALCJNRAAVD 245
QY 136 --OVSVPFLWAAGRHADVHLLMLQKAKVNSCKYGTTPLVWAARKG----- 182
Db 246 FTARNLTPHVAHINHLINIVKILPS LRIHSDPAWVYTHIAPKQVQVPSLLQYAG 626

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Introns: 814/1

C:Superfamily: ankmyrin repeat domain

C:Keywords: alternative splicing

Query Match

Best local similarity 20.4% (E=1.0e-10) (100.0% 100.0%)

Matches 426: Conservative 200: Moderate 64: Distant 64: Gap 85:

QY	24	REENTALKALIEKTKYKQKESKECHQETIMLAGQVYVLLVLENDALWLEDELR	918	EELLVPSKHOHLTFTRLEFSDSJRHYSWAADTLDNVNLSVSPVHSGFLVSEYVARG---	974
DB	66	KEGVVEVSELEQREANVPAATKQNTALAFALACAEVAVVWVWVWVWVWVWVWV	715	VLDLKLKSG---	741
QY	74	ALISASKEGHILVLEHLLKSSALSLRPVWMLAKWAVEFTVAVLEL	975	GSMSQSPHSGMRLIIPPKTAPTRITCLVKRHLKLANPPVWVEGEGLASRLVEMGPA	1032
DB	126	PSTYAAQENHLVVRFLDRGASQALAEQVTLAVALQCHGVVSLLENKTKAVE	742	FMKVLCREVELMARMAKTIDSTFQNG-----TRLVVIDGLDACEC	782
QY	125	-----SHVAVSVVGL	1233	GAQFLGVVYVLIPIHEGSMRQKREELVLRSENGRTWKEHOFDSKNECLAEAGNOMO--EE	1090
DB	186	LPALHAAEKDQTKAAMLLQNTSGRQESKSEFTPHANAVYGVINVAILLERAGAVD	993	DKVQMLDTPV--DSKQDFEAFASCPRIIKAINQNLNSVLDRDSNIGHVYRNVIVH	840
QY	195	-----	1291	LSPEELGTRICWIKKDFCYFA--VYVRKQESNQIQEGG!	1133
DB	246	FTARNDITPQVASKRQNAWKLLOSARKTAKTEGELTETHTGARGSHQVTEKLD	841	LPVFUNGSGNAARKFYTSATNGNITCSTTQTQ-----EDTRRVSONSLGEMTKLG	894
QY	193	-----HPTVHLLAVTQVQVQVRSYVALVAVKNTON	1134	LSSTTVLVOASFPEGALTKRIRVCLQAPVPEETVKKI-----LG	1174
DB	306	RSAPILSKTKNGLSPUNVATQDHNVALELCHGVVAVPTVAVTALVAVAGHYKV	895	SKTALNRPLTYARRQVQRTIIRQMSFDIKLL-----VTEDWFSDISPQTRRLINIVSV	949
QY	210	VKEHLKERNVNLTKDQNTALMIASKE	1175	NKATPSTVTVPEPRKFKHPIT--MTIPVPPSGGVSNYGKDATPNC--RL--CS:	1228
DB	366	AKVLLAKASPAKALNKPURIAKKAAPKQKLLKESLQNTQESKTPHINAAE	950	TS-----ELLRANOITENWDLASWLNTECPVYRTSWL-----ILV:EELEGLPQ	996
QY	249	GHREIVDOLLAGTYVNFDRSGVLLIMKAPDQVEIVRAIISYVALDPRQNTA	1229	TSQSPQAGWITGTPTRKQCVSTTNVSAFP-----WLADCHQVL--ETVGLASQ	1280
DB	426	MGVNVVSGLNHHGASPTNVKRGHETALIMDAEIKAAVVEVWVQVWQVWQVQVQV	997	MTLKTMYFRISKNPITTKQVEPILEGGDIRNF-----EYFLSRT	1037
QY	307	LYWAVEKGNATVVRDILQNTPEHTEKSTHLLPATKMEHLLPVEHLLKQAVSAE	1281	LYRELICVPAWAKVFAKTNCP--VESSLRCFCMTDORVDKTKLEQCEEFVARSKDI	1337
DB	486	LHISAPKADIVQCLQCGASPMATDQNTYTHLGAPEHLEVAAPLHUGASLSIT	1038	PVILVARDVFLPCTVNLDPKLR--ELIADVRAPE-----QINIGLAYPPLP--L	1085
QY	367	KKQDTTHVAIRQESPPALALP	1338	FVLSQKFIYVDCVGNLAPLTGKGCQVFNFYFKEKRLPFSIKIRDTSGPCGRJSL	1395
DB	546	KKQFTLHVAAYVGRLEVAALQVAPLAAQVAPLAAQVAPLAAQVAPLAAQVAP	1056	HEGPRPESVYQSPASVSSASPNQPFEGVVSQPHSSVYSGSGPOHPFNRAAVFAT	1145
QY	394	YRILEAGRELYNITSSALALAL	1396	KE--PKTKIKPQTA--VCN-----LNTLPARKKAKKADARQS	1430
DB	606	SEMAAKRGVTHHIAFRRQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV	1146	GSSLLD-----SSNTVDVWCKELQREGLDQNMPOYCTTIKKANINGRLVSC	1394
QY	442	DLYSSALADILSEPTNQ	1431	PASIALPKFYVLTPEVSNFQSPQERTDIRVAIVADHLGLSKTELARELNFVDENQ	1489
DB	666	LGRNAVNLNKSQUTPHILAAQERVVAVVAVVAVVAVVAVVAVVAVVAVVAVV	1195	NIDELKREYANHF--GDW-----HFRSMVLEMRSVESQVVPEDP	1232
QY	470	GSQK--SFLIK--KLEDEKTPAQTCTHCLPQKLVPEL	1490	EVENPNSHLLAFPMLEKRWTRDGRNATLALTVLTKINPDIIVTLEGGHIFQYCN	1549
DB	724	GNIKVNFLLQSAKVNATKQCYTALHAAQKTHLLVWV--KVASHELTNG	1233	PELHNER--GAVVGRJESAPPSHLELFTLQSSCTPYTLNFSFERNLGLDQAPR	1288
QY	517	FAPVDTKLAIALISLFLALVYPIV	1592	IKSPALPMDGHDV--DGR--HFOVELETNMGVYWT--PQNFQDQD--H	1593
DB	780	-----NTALAPRLVYVSVDTLVVTRIMNTITTEKURVLAETNCEVLNSED	1253	HSNLSKQVLEHPTPSLSS-----LNSQSSSEISKTKV--QA	1325
QY	553	ESNNKAWALSTRARHIGYILELLEPK	1594	ISDISSLEHPTPSLSDGLVPSQGNIEHTGPPVVTAEOTSLDSKMDSVTVDPA	1653
DB	935	CKCTWKPKVQ-----EVLVAKALVETRYLGLPGLKEGDSQSE	1326	EYRDVAYPIVQMSQEGTSSISG-----RSSP--HSTYVIGQSSSGSHSTLEQ	1377
QY	604	NRLSSVGGTSLAEVATLSCACEREGFATREVERTEESQKKKKKCCCLPSEVI	1654	PLVYDESCADLCQSECAQCMASVPGIPNCGRAEPLRPQTRKVMGSE-----Q	1705
DB	891	---GYVG--FSLGARSASR-----SPSSSESYTLNPSFTRP-----QSKV	1378	EPGKECELKJSDGRKSPVFKSGDV--DVSSSGVSTKEASPLDPIITEDEKSCSCSKLPG	1437
QY	664	PLFVGGIAGITLALAFVPEPKHPT-----VNAILLASVVGIAFVLNFTWQ	1706	EKGKSG-----PDEVTEDKVK-----	1722
			1436	KKSSRPRLFTDLKLKQGLRYQKLPKDESGTGRVQITPHCSKQIRTKRLKAKQRE	1497
			1723	-----SLFECLQLE--EVEAEEMTEDQCAMLRVQ-----RAELAMSSLAGWQNET	1767
			1498	ASPOEHSAPETFTFIKAYLSLDALLQKKSSDSDSVRSN-----ESSPNHSH	1545
			1768	BSGSLSPAAR-----LTGGLDLRLDSSDCARDSITSYLTGEPCKTEANGNHT--	1818
			1546	NFAADESQLEKLVNLEDEGHSGKRGV-----PHSLGLQDPIIARMS:CEBCKXSP	1598
			1819	--AEVIFAPAKPYFESQND:GKQSIKENLKPCTHOCGRTEBPV-----SPLTAYQKSL	1871

1249 TGGTSPAQWEDI.....TGTPATFKKCVSPF.....CTNV -SAPFNLADCHQVLETVG 1296
QY 1075 IGRAYAPPLFLHGPFRPPSGYSGQASVSSANFNQPPFGQVVSQPHUSYSYGLSGPCH 1334
Db 1297 LATCYLRECC.....LV.....PRKAKV 1323
QY 1135 PPKYPAAPATGSSALLSNTVDVAPEKRCIEILQNYKYPYVYTIKMANINPVLSOT 1194
Db 1124 -- VESASRCFNTUQKPVKYLEQQ 1346
QY 1115 NIDELAKKAKNFGWHFESMVLEKPVESQVFQPPREYENNSAIVHGE 1248
Db 1347 NFEVARSTCEVLEKPIVLYTCHALCTKGGQOLVEN 1386
QY 1249 ARSSUSHELTELSQCTPYLNRFEELNGLDSEKAPRHLKAKVQTRTPD 1304
Db 1387 FYSFRENLPFSIKITQCEPQPLSEKERTTQGLPOTAVNUNKTUPAKKETER 1445
QY 1305 SSIKSGDSSIEISKUTKVCVAYEIVYV YIAQVQLE NIKHSTISJSSPSHSTYV 1361
Db 1446 ----DODDEIE- KTDRCSPASALPFRYSYLSRQMIERTSTAT PSLP TTY 1492
QY 1342 IGGSSSGSTHTLSEBFGHGLVLELHRYSTHMRGVVGVSSSVGVTGASPLQPT 1421
Db 1493 ----SYKPFSGRIYQSWTAPITV HAKS QFTLSSASNTVQASPLSTW 1541
QY 1422 EHEKSLGSSKALPDKKSEKESLPTDKLKTPLPQCTGTFLEHCHRNQITPHC 1481
Db 1542 -- ----SVSTSPFASLGASTHGVKISCV 1567
QY 1442 SKVITRRKAKQREKASQEHSAEPIFKAKVLSKALLKRLS 1528
Db 1548 ASPIRLRTMSKTKVSSQPNVYVSLASAVHEATPLK 1614
QY 1529 SCSQVKNSSFNHNEAADSLEKALILELHGNHKEKRYOS 1576
Db 1615 ASKSTSSRFSF...VTTAGSLSEKSLNTEFASKSNVYSSSPFKSITTSAA 1668
QY 1577 ----LSGLQDPIARKSLCESEFPKFNKASPEKNA..... 1614
Db 1669 PLASEPKSVSVKGVYVSSAPVMSGSS...SSPAKQVGHASVAVNGSISFLY 1725
QY 1615 CUKAYNLNRPESTVTKNN-TAPENQD...KPELEIGHETSQV -LEPQSPR 1665
Db 1726 ASSTTINCKKATATCEKLSHATNVSVSALTFVKEVSTTAKVPELESYSAA 1795
QY 1666 PTAVMENKSVAPRQPSSTYVYVAGHAGASPT 1748
Db 1746 PSAPUSLEUNAS 1795
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S37771
ankyrin, erythrocyte -ouse
C:Species: Mus musculus (house mouse)
C:Date: 27-May-1994 #sequence revision 13 Aug 1994 Bank change 13-Aug 1999
C:Accession: S37771
R:Birkenmeier, C.S.; White, R.A.; Peters, J.L.; Hall, E.E.; Iak, S.E.; Barker, C.E.
J. Biol. Chem. 269, 9533-9540, 1994
A:Title: Complex patterns of sequence variation and duplication 5' and 3' ends are found an
A:Reference number: S37771; NID:6325853; PMID:844664
A:Accession: S37771
A>Status: preliminary
A:Molecule type: mRNA
A:Accession: 1-1848 <BIR>
A:Cross-references: EMBL:X69063; NID:631815; FIDR:CAATB00117; PID:g311817
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
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F:61-111/Domain: ankyrin repeat homology <AN02>
F:114-146/Domain: ankyrin repeat homology <AN03>
F:147-175/Domain: ankyrin repeat homology <AN04>
F:176-208/Domain: ankyrin repeat homology <AN05>

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F:473-505/Domain: ankyrin repeat homology <AN14>
F:506-538/Domain: ankyrin repeat homology <AN15>
F:539-571/Domain: ankyrin repeat homology <AN16>
F:572-604/Domain: ankyrin repeat homology <AN17>
F:605-637/Domain: ankyrin repeat homology <AN18>
F:638-670/Domain: ankyrin repeat homology <AN19>
F:671-703/Domain: ankyrin repeat homology <AN20>
F:704-736/Domain: ankyrin repeat homology <AN21>
F:737-769/Domain: ankyrin repeat homology <AN22>
F:770-802/Domain: ankyrin repeat homology <AN23>
Query Match 5.8%; Score 516.5; DB 2; Length 1848;
Best Local Similarity 19.6%; Pred No. 7.8e-22;
Matches 397; Conservative 281; Mismatches 651; Indels 697; Gaps 81;
QY 21 LKALLEKTEYDENECCQTPMLAAEQGNVBIUKELLGKANGCNLELDNWTALISASK 80
Db 96 VRELNVNANNVNAOSQKFTPLVYAAQENHLEVKLENGANQNVATEDGFTPLVALQ 157
QY 81 EGH - 83
Db 148 OHENNVNHLINYGTKGVRLPALHIAARNDOTRTAAVLNLDNPNPDVLSKTGFTPLHIA 217
QY 84 -----HVEVELKSGASLEHRMGSGMTALMKACYKGRDVEVELLSHGANSVVGLOYS 138
Db 218 AHYENLVNACGLLARGASVNFTPQNS:TPHIAHPRGNVIVVRLLCRGACIE IRTKDE 276
QY 139 YYPITMAA IPHADIIVHLLQNGAKVNSQYGTTPLVWAARKGHLECKVHLLJANGAVD 198
Db 277 LTPHCAAKRHVRISILLDHGAPIQAKTKNGLSPIHMAAGGCHDCVRLLOQYNABID 336
QY 199 -----QESA-----NSMTALVAVKGGVTCQSVKEILK 225
Db 337 DITLDHLITLHVAAFCGHRHVAKVLLQKAGKPNRSLNGFTPLHACKNH:RVNMLJLK 396
QY 226 RPNVNLTKQKQNTALNIAKSEGHIEIVOCLLDAGTYVNIIDRSQGTVLIGAVRGHVEI 285
Db 397 TQASIDAV ENLTLTVVASENGHLPIVKNLQFCASPNVSVKVEITPLVAAARAGHTEV 456
QY 344 VPALICFYVLDIPQGNKNTALYWAVEKGNATKWTLOCNPDTEICTKQSTPLIKATK 345
Db 459 AKVLLQKPKAKAKAKQDOTPLNCAARIQHTGCVKLLLENGASPNLATTAGHTPCHTAAR 516
QY 346 MRNI BWVELLQKGAQVAVDKKGTPLHVA:RGRSRLAEILLNPKDGRLLYRPNKAG 405
Db 517 RGHVDITALLLEKFAESQACTKKGTPLHVAKYKVRLAELLEHDA-----HPNAG 570
QY 406 E---TPYNLQVSHQ-----KSIL-----TQIFGAR----- 427
Db 521 KNGLTPHIAVHNHNLDIVKULLPRGSPHSPANNGYTPHIAAKQNCQIEVARSILQYGG 630
QY 428 -----HUSPTETDGMCGYOLYSALADILSEPTMQP-----PIC- 462
Db 631 SANASVQVTPPLHAAQEGHTEMVALLSKQANGNCGNKSGLTPLHLSVQEGHVPVADV 690
QY 463 -----VGLYAQWGSCK--SFLTKKLED-EMKTFAGQOTPELPQFQSWL 501
Db 691 LKHGVTVVATRMGYTPHVAHYSHYIKVVKVFLQHQADVNAKTKGY--SPHQAAQQ 748
QY 502 --IVFELTLCTGGGLVLPAPPD-----TNLAIAISLSFLALIVIFFIVYFGGRREG 553
Db 749 GHTD:VTL-----KNG-----ASPNVSSNGTTPLAIAKRLGY:SVTVOLVKVT----- 794
QY 554 SWNKAWS:PLARHIGYLELLFKLMFVNPPPECTTKALPV---RFLFTDYNRLSS-- 608

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2	650	6.2	374	ANK2_MOUSE
3	577.5	6.0	1952	ANK2_MOUSE
4	426	5.9	4377	ANK3_HUMAN
5	468	5.3	768	ANK3_HUMAN
6	471.5	4.9	1049	ANK3_HUMAN
7	474.5	4.3	1411	ANK3_HUMAN
8	466.5	4.4	1411	ANK3_HUMAN
9	464.5	4.4	1416	ANK3_HUMAN
10	464.5	4.4	1416	ANK3_HUMAN
11	474.5	4.3	427	ANK3_MOUSE
12	460	4.1	874	ANK3_MOUSE
13	477.5	4.2	741	ANK4_HUMAN
14	466	4.0	735	ANK4_HUMAN
15	442.5	3.9	622	ANK6_HUMAN
16	437	3.8	1267	ANK6_HUMAN
17	435	3.8	1401	ANK6_HUMAN
18	431	3.7	525	ASB1_MOUSE
19	429	3.7	583	AS15_MOUSE
20	438.5	3.7	516	AS33_HUMAN
21	434.5	3.7	747	V242_F_MV
22	417.5	3.3	542	V155_F_MV
23	403	3.2	624	V244_F_MV
24	408	3.2	536	V024_F_MV
25	407	3.3	436	V245_F_MV
26	428	3.3	525	V228_F_MV
27	488	3.3	1083	V102_FHSM
28	495	3.2	1210	BAG3_HUMAN
29	484	3.2	1243	BAG3_MOUSE
30	474	3.2	592	V246_F_MV
31	470	3.0	603	V162_F_MV
32	474.5	3.0	414	AS15_HUMAN
33	474.5	3.0	656	F53_MOUSE

605 ISIAVVGGLAFV...NRTWK QVELLSLNSQKSHSAASKLRL 737
 616 IROSAVDCVWVPSHOVSTLAKAEHNSVLSKWTENKCLWALS...SSPIR 965
 738 KSEDFKVLKCEVELMARKTIDFTNCTPFWVJTGGLACQKVLNLTQVRLVS 737
 744 SGLVFWVDAR...DQAKMS FSHNGIR ILLPFTAPTRVLPKAPRRLAT 1016
 745 KQPIALFASDPIILKALQNLKAGKCHNGHGWYRN IIR PVELLSE FSNKAGF 556
 1017 MFRVVE...FGLAKR FVHAGACFQVTVVTHFASIF 1562
 867 LVSATNDEL...CSQVNTGCTATFVSAQHLNENKLFNADNRETHERRNCP 912
 1022 VVLSGKDSWALHFCVY...FLLNENLN SGEVU FHEDEKKEKLP 1108
 913 TITQNFEDLTVTEWESDINSQKAEKLNIVSTFELAN...CTFKNRDLA 957
 1109 IETDF...DQFVAVVS FIKOTSKLIGSGVLSSTVPLVAVFEGAL 1156
 968 SWNLTEQWYFWSMLDYLEETELDCNT...KIVYERSKYFETK DYER 1519
 1147 KTRVGLQAFVHSELVKILGNKATSPVLTLEPFRHHKI...MTIPKASSDV 1215
 1000 LEINDGIRNFV...SSSTFVIVAPKNTCTVVALPPKURELIAC 1565
 1216 NGVDEAPTRILISITSGT-PACKHEDTNTTETVNEVSEF TTAG...ARFSLID 1290
 1366 VEARREINLQVLPPLHSHVFFLSVH LQAVTSRQF...FFLVVAPQWESY 1125
 1371 QROTQSVTASGVYRI...V...VFMK 1296
 1164 VVAGLGHCHPFAFMAVPAFSSLSLSVTVGVNCPQVGLQVWVCTFKKAN 1185
 1297 FVFAKSHDPIEN...HPEVMTGKNTCTIC QVREVASPIVEV 1342
 1164 INR VLSCQ...NDEKAEKAMNE GMLFPRVVLNENYEVAVPEFENKSAF 1342
 1343 LEKPIVDCVGNVPLTK...QHINPLAK FQV LEPVAVNTQ 1389
 1243 VVHESARRSHLPDTELSQCTITNFEELTLEHRAKQV... 1332
 1200 ETLR...LSENEKNTCTVLA QHNTCTVTFESE 1427
 1243 SMOGJRTPTSLNSQNSISIEFALTKVAGVVD APEV...NLFHGSSTIS 1351
 1414 SGLAEHLMKQKNDPSTETCTFQHNDVYVH...HNDV... 1285
 1452 GNSHPIYV...SINIEH... 1476
 1416...ALITLQKASIKV... 1444
 1427 SUSTNASHPLA...THE... 1437
 1594 SGTCTOESVAGVSPSEJFVRESEVNTSLEF EAPVAFAL...EVNCTVDEBIF 1534
 1418 KKSSEBS...FGV... 1468
 1594 KVEKSTVUNYINDNTVTPHPLTV... 1554
 1469 ESTGVQVCTTH YEMARTVDFVAF... 1528
 1455 QSTOKHKPSGLIKPKV...K... 1499
 1129 SSSVPRNESSPNISLINEADOSLE... 1377
 1500 SEESMERPPGLARPLCPVATSC... 1759
 1578 SGLDPIIARNS...SEKKKSPSE... 1437
 1594 KGRID...VPKTHRI... 1502
 1618 NKAQNTETELSGPETSQVILRP... 1516

Db 1803 SAKTERHVPSSSKTEK...KTERHSPASSSXT-----E 1643
 QY 1697 LHAASSET 1705
 Db 1844 KUSVAPR 1852
 RESULT 1
 ANKI_MOUSE STANDARD; PRT: 1862 AA.
 AC Q2487;
 DT 01 NOV 1995 (Ref. 1, Created)
 DT 21 NOV 1995 (Ref. 2, Last sequence update)
 DT 16 OCT 2001 (Ref. 4, Last annotation update)
 DE Ankyrin (Erythrocyte ankyrin).
 GN ANKI OR ANK-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID:10090.
 RN 1.
 RP SEQUENCE FROM N.A.
 RC TISSUE=Erythrocyte;
 RX MEDLINE=92345717; PubMed=1386265;
 RA White R.A., Birkmeier C.S., Peters L.S., Barker J.E., Lux S.E.;
 RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
 RT regulatory domain".
 RJ Mol. Genome 3:294-295(1992).
 CC 1. FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
 CC ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
 CC NA-K ATPASE, TO THE LYMPOCYTE MEMBRANE PROTEIN GP85, AND TO THE
 CC CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
 CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
 CC CYTOSKELETAL CHAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
 CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
 CC 2. SUBCELLULAR LOCATION: CYTOSOL; CYTOSOLIC SURFACE OF ERYTHROCYTE
 CC PLASMA MEMBRANE.
 CC 3. PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
 CC 4. PTM: ACYLATED BY PALMITIC ACID GROUPS (BY SIMILARITY).
 CC 5. SIMILARITY: CONTAINS 23 ANK repeats.
 CC 6. SIMILARITY: CONTAINS 1 death domain.
 CC THE SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@ebi.ac.uk).
 DR BNP1, M81756; A00011, J411;
 DR PIP, I49502; I49502;
 DR RSGP, Q00420; I49502;
 DR MGC, M3189024; Anki
 DR InterPro: IPR002110; ANK
 DR InterPro: IPR002448; Death
 DR InterPro: IPR002446; ZUS.
 DR Pfam: PF00223; Ank_14
 DR Pfam: PF00531; G3a1n_1
 DR Pfam: PF00791; ZUS_1
 DR PRINTS: PR01415; ANKYRIN.
 DR SMART: SM00245; ANK_22
 DR SMART: SM00005; DEATH_1
 DR SMART: SM00218; ZUS_1
 DR SMART: SM00098; ANK_REPEAT_20.
 DR PROSITE: PS0098; ANK_REPEAT_1.
 DR PROSITE: PS00297; ANK_REPEAT_REGION_1.
 DR PROSITE: PS00017; DEATH_DOMAIN_1.
 KK Cytoskeleton; 5-(ank)-ANK repeat; Phosphorylation; Lipoprotein.
 FT DOMAIN 1 1-23
 FT 89 kDa DOMAIN (ANION EXCHANGE PROTEIN
 FT BINDING DOMAIN).
 FT 62 kDa DOMAIN (SPECTRIN BINDING
 FT DOMAIN).

1498 REYS:SPSONGSS:QDELLSPAS:CYALP SP:ALCQWKEVTVDAI:LAATERSTM 1556
1446 IFOTOLKKGGLRKYXJSDDEDTTQVQTPHSDMPTA:KARNS:GASQEHSA 1505
1557 LEMSONQVASAGLT:PSLVTAEDSS
1566 EP:RTIRAKAYEL:ALLKKSSE:IN:ENE:SPHRI:AD:AND:PEEL:PAVIL:IED 1564
1592 IP:..... ENKLE:RISE:IN:QUE:PSUVE:ED:SD:AT:LA:JUSEP 1637
1565 KORSKE:MPHSI:SUQU:DIAM:INSKOKY SP:..... 1604
1538 GGS:ANK ROEVS:TEQO:FEV:VNS:AL:GHN:AD:IOSI:VE:VLD:AS:IL:MTQ 1695
1674 ---AN:PER---SW PA:QAY:LINE:ISTV:ING:AF:IRAN:Q:VEI 1647
1596 GST:AV:PO:ATOS:WOF:ETQPH:PO:R:TTI WH:EM:AL:CE:VE:CV:V:STR:RY 1750
1548 -EUI:RTSQV:LRP:SP:ENPTA--- VONEN:K:MA:K:VE:Q:PS:VT 1588
1751 OR:PP:ETSP---KAG:ERS:MA:PE:AS:PE:VO:CH:EL:ON:PS:RO:VE:EQ: 1738
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AC Q12955, 2003 (Ref: 41, Genbank:
DT 28-FEB-2003 (Ref: 41, Last sequence update:
DE 28-FEB-2003 (Ref: 41, Last annotation update:
DE Ankyrin 3 (ANK-3) (Ankyrin 3)
GN ANK3
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homin
GX NCBI TaxID:9606,
FN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain SV40;
EX MEDLINE:9511a209, PubMed:763469,
FA Kordeli E., Leberer S., Bennett V.,
RT "Ankyrin6, A new ankyrin gene with local specific isoforms localized
PL at the axonal initial segment and cell of Schwann",
J. Biol. Chem. 270:2332-2359,1995,
CC FUNCTION: Membrane-cytoskeleton linker.
CC ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing, 2 isoforms identified.
CC Comment: A cluster of 28 genes is present
Name=1
Isoid Cloned in September 1995.
CC TISSUE SPECIFICITY: Expressed in brain and Schwann cells.
CC SIMILARITY: Contains 23 ANK repeats.
CC SIMILARITY: Contains 1 death domain.
CC This Swiss-Prot entry is copyrighted. It is distributed through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL database.
CC the European Bioinformatics Institute and its restrictions on its
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modified and this statement is not removed. Usage by any other commercial
entity requires a license agreement (see http://www.ebi.ac.uk/announce/
or send an email to license@ebi.ac.uk).
EMBL: U13616; ANK64934.1;
PIR: A55575; A55575.
HSSP: P56273; 1E18.
Genbank: NC01494; ANK3.
MW: 603465.1;
GO: GO:0006605; P:protein target; I: NAS.
InterPro: IPR002110; ANK.
InterPro: IPR005488; Death.
InterPro: IPR003906; ZUS.
Pfam: PF00021; ank; 24.

Pfam: PF00531; death; 1.
Pfam: PF00791; ZUS; 1.
SMART: SM00248; ANK; 21.
SMART: SM00025; DEATH; 1.
SMART: SM00218; ZUS; 1.
PROSITE: PSS0086; ANK_REPEAT; 21.
PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
PROSITE: PSS0017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat.
FT REPEAT 73 102 ANK 1
FT REPEAT 106 135 ANK 2
FT REPEAT 139 168 ANK 3
FT REPEAT 172 201 ANK 4
FT REPEAT 203 230 ANK 5
FT REPEAT 234 263 ANK 6
FT REPEAT 267 296 ANK 7
FT REPEAT 300 329 ANK 8
FT REPEAT 333 362 ANK 9
FT REPEAT 366 395 ANK 10
FT REPEAT 399 428 ANK 11
FT REPEAT 432 461 ANK 12
FT REPEAT 465 494 ANK 13
FT REPEAT 498 527 ANK 14
FT REPEAT 531 560 ANK 15
FT REPEAT 564 593 ANK 16
FT REPEAT 597 626 ANK 17
FT REPEAT 630 659 ANK 18
FT REPEAT 663 692 ANK 19
FT REPEAT 696 725 ANK 20
FT REPEAT 729 758 ANK 21
FT REPEAT 762 791 ANK 22
FT REPEAT 795 825 ANK 23
FT DOMAIN 1519 1498 SER-RICH
FT DOMAIN 4032 4174 DEATH
SQ SEQUENCE 4377 AA; 480339 MW, 54237955768B684 CRC64;
Query Match 5.9%; Score 526; DB 1; Length 4177;
Best Local Similarity 20.0%; Pred. No. 1.9e-19;
Matches 416; Conservative 266; Mismatches 664; Indels 734; Gaps 80;
QY 14 KENT:PAK:KALLERCKEYDNERNECQTPIM:AAFGCNVEIUKELLKGCANGLDLENT 73
DB H3 KEGYVEVVEH:LOREANYDAATKONTALH:AS:AGQAEVVKVLVTNGANNVNAOSQGT 142
QY 74 ALISASKE:R:H:IVERE:IKSGASLEH:R:MGOWTAL:YWACYK:GRT:DWELL:..... 124
DB 143 FLYMAD:CH:LEWZ:FE:LENCAS:SLATEDGTP:LAVALQOQHDCQV:SLLENDTKGVK 202
QY 123 -SHGANPSVTG: 135
DB 203 JFALH:AA:V:TKAAVLLLOKNNADVESKGF:PI:HAAYGN:IN:VATL:LNRAA:VD 262
QY 136 ---QYSV:PI:K:AG:CH:AD:IV:ELL:LONGAKVNCSDKYGTTPLVWAARKG..... 182
DB 263 FPARND:PI:CH:WASK:GN:AMVKK:LD:RGAK:DAKTRDGLTP:LCGASRGHEQVVEMLJD 322
QY 183 H:ECVKG:ILAMGADV:DCGANSMTAL:IVAVKGYGTS 219
DB 323 RAAPILSK:K:GL:SP:LMAT:QDH:LN:CYO:LL:LOHNPV:VDYD:VNDYLTAL:HV:AA:HG:YKV 382
QY 210 VKETIKRIN:V:NT:DK:ONTALM:ASKE 247
DB 393 AKVLLDKV:AN:KAKALNGT:PLH:IAKKNP:KVMELL:LLKHGAS:ICAV:ESGLTP:HV:AA: 442
QY 248 CH:EI:V:OLL:LDAGTYVNI:PO:RS:GDTVLIGVRGCH:VEI:V:ALLQKYAD:IDIRGDNKTA 306
DB 443 MGRVNI:VS:QIMH:GASPN:TNV:RG:ETAL:HP:MA:RSQAEV:RYLV:QD:GAQV:AKAK:DDTP 502
QY 307 LYWAVEKGNAT:WVR:ILO: CNPOT:..... EICT 333
DB 503 LHISAR:LS:AL:IV:OOL:COGASPNAT:SGYTP:PLSAREGHEDVAAP:LLDHGASL:ITT 562
QY 334 KGGETE:PL:VA:EMRNI:EV:VEL:LLJKGAKV:SAVDKKGDTPL:HV:AT:IG:RSRR:JAELLRNPK 393

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DB 1387 FYSFKENRIPPSIKINDTSRCPGRUSFUKERKTTKGLPOTAVCNUNITLPAHKKTES- 445
QY 1305 SSINSQCSSTESKLTQKQCAEVRDAYRE---YIAQMSOLEGCTGSSTSGRASSPHSTYY 1161
DB 1446 DGRILYRNKAGETPYNDCSHKSLTQFUAR--RLSPETSGDM 438
DB 1446 DQDELEZ KTDRECSFASIALAKRYSVTEPGMIERSTGAT---RSLP-TTV- 1492
QY 1362 IGOSSSSGSHRTLBOERKKESELKQEDFKKFLKXRGQVIDYSSSGVSTNEASPLDPTT 1421
DB 1493 SYKFFETPPVQSWTTAPITVPGPAKS---GFTSLSSSSSTPSASPLKSIW 1541
QY 1422 EDEKEDJSAKLLPKKSSSRSLPOTDLKLKGGJLRQKLPQDEDESGTGRVCITPHC 1481
DB 1542 SVSTPSIKSTL-----GASTTSVKXSISDV 1567
QY 1482 SKVIRTKRLKAKGECASQCHSAEPIRTIRAKKEY---LSDALLDK-----KDS 1528
DB 1568 ASPIRSLPT--XSSPIKTVSQSPYNIQVSSGTLARAPVTEATPLKGL 1614
QY 1529 SSGVSRNKAQKRIHSHUHNAAJDSOLEKANLIEDEGHSGKRGMPHS--- 1576
DB 1615 ASNSTESSWTP-----VTTAGSLIERSSTITMTFASPKSNINMYSSSLPEKS:ITSAA 1668
QY 1577 LSJLQDFLIARMSICSDKKSPCECSLIASSPEESMTA----- 1614
DB 1669 PLISSPKKSVTPKSRGVVISAKITMASS---SSPKQKPGHAEVALVNGS:SPLY 1725
QY 1615 CQKAYKLRRTTITVLNN-TAPTNRANQ---NDEIEGIRETSQVI---LRQPSPM 1665
DB 1726 ASSTL:KCKATATLQKISSATNSVSSVSAATTVKVFSTTTAMPFSLRSVVSAA 1785
QY 1666 PRAYONENKNNHKSQSSSYTRLSKQASEIHAASSEST 1705
DB 1786 PSAFOGSRKTPAS--ALYTSL--SSSISATTSVVT 1816

RESULT 5
YE23_HUMAN ID YE23_HUMAN STANDARD, PRT; 768 AA.
AC Q9ULQ7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DR Hypothetical protein KIAA1223 (Fragment);
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
EN NP_174109.60;
EK 1;
RP SEQUENCE FROM KIAA
RC TISSUE-BRAIN;
RX MEDLINE:20039619; PubMed:12574462;
RA Nagase T., Ishikawa K., Kikuno M., Hirotsawa M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain: which code
RL DNA Res. 6:337-345, 1999).
CC -! SIMILARITY: Consains at least 14 ANK repeats.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AB033049, BAA66537.1;
DR HSSP: P42771; LOC2
DR InterPro: IPR002110; ANK
DR Pfam: PF00023; ank_14
DR PRINTS: PRG1415; ANKPRIN

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DB 363 KKGETPLVAAYKQKLEVANLLQFNSAPDAAGKSGULTLWVAHYDQCAVALLL---D 619
QY 134 DGRILYRNKAGETPYNDCSHKSLTQFUAR--RLSPETSGDM 438
DB 620 QGASHHAAAGGYPLHFAAKNCTGDIATLLEYSANANATVQSIASHTLAAVEHVN 619
QY 439 LQYHLYSALACHILSEPTECP--- 466
DB 680 VSLLEHMANVNLAKSKSLTFLHAGAGLRCTVALVNLQDQKLAFTATVYTCWACH 439
QY 467 AGWISAKK--SELLK-KLEKEMTATLCTETEPFNSKL--LPELEK--HMLVFAFP 520
DB 740 --VGIKIVRFLLQSAVNAKATNY--FLHGAAGQMHFIHVLNAN--ASPN 790
QY 611 -NCTLALIA:LSLFCALIVIFIVIVGKRAE:RSHWKNALSTLAPHLVLELLEK 577
DB 691 ELYVNGNTAKG:----- 814
QY 678 LQPV--NPPE--LPQCTKALPVALETTYKPKSV:GGET 613
DB 815 LK:VTEHNTVTTVERKKNVPLVWREVKMATEVEFKAKAPKNSGQSVIGWEEGED 874
QY 614 SCA-----EMIATLSKCEP:LFATPQ--PPEVTEHSCAKKPKWKTQD 659
DB 875 ANTOSTAYLQFQQLKEGQSDLAEGIMJFGLQARVASLQSPERSQATLNLHSSYAR 912
QY 659 PNPVFLPIVAGIAGITLAIFFLITPQT--AGALDIAAVYLAFLNLS 709
DB 913 DSNV:HELVSKKELTETPEFLAKN:RHSKALTLQWVLSAPLS:FLDSEFWA 992
QY 710 RTWQVITSLNSPKR:LSAASV--HLLA:ELPQVAV--KPEVEMKAWPT:ESFIQ 769
DB 993 RG--GVSGSSPHSG--NELLTP:EEETAL-- 1010
QY 766 NOTELAVV:IDGLDA:TEQKRV:QMLQ--VSGTPE:RFFAIFNSCHQITL:FEALN:QKNSVL 825
DB 1020 ITCALV--KHEKLAN--EPG--ELPSPHSSKLV 1047
QY 836 LSNUNHJMYMAN--VHLVPVNS--GSHKKEV:VLA:AGKQKQKQKQKQKQKQKQKQKQKQ 884
DB 1048 EMGAGAGAGFQSV:VEIPRHPMS--PERE:VIRSELPQ--QWPHLPD--SK 1036
QY 845 NSLQEM:KL--GSTALKERTYK:VQVTRTIR:EMGAGAGFQSV:VEIPRHPMS--QWPH 942
DB 1097 NS--NELLQNGM:PELQSEEL:QV:ELIIF--KGLAVES--HIFQ 1142
QY 843 LEMVNR:KSLQIRP--LQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 977
DB 1043 EMLQ:KPEHISQ:TVL--LQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 1149
QY 908 TLTKV--LQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 1042
DB 1199 VKRLKRAKATESP:VTFIRKAKSKNLTML:LL:ELISJE:ALN:WNV:TEHNSLQSI 1249
QY 1023 EQ--DIRNFEVFLSETHVAVAW:WFLH:FTQL:IPTR:ELIACV:WAEQ:IN 1074
DB 1049 TQSTSFACWED:-----TQSTLQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 1296
QY 1015 LQELAVV:FLHECP:PPRPPSSQ:LAQ:SNVA:RSHLO:QKQKQKQKQKQKQKQKQKQKQKQKQ 1134
DB 1077 LATQ:YFEL-----LV--FIVAEV--VEAKN:LP 1323
QY 1145 PYNNAV:PATSSILASSVTVQV--EAP:QK:ELQNDQ:VY:VTF:FEAKN:IRVLQSC 1194
DB 1344-----VESSLRCTQVTDQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQ 1346
QY 1195 NIDECKKEMANFGDWH:FRSNV:KRVAVESQ:WERTPEFL:FNSSAFVHGE-----S 1246
DB 1047 NFEV----- 1346
QY 1043 APRESHT:ELP---LTSLSQCTPY--LNSPFRNTLQ:LEEMPHNSL:WALS:LTRYSL 1304

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DR SMART: SMO0248; ANK; 13.
DR PROSITE: PS00088; ANK REPEAT; 13.
DR PROSITE: PS00297; ANK REP REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat.
FT NON TER 1
FT REPEAT 1 1; ANK 13
FT REPEAT 15 44 ANK 4
FT REPEAT 45 63 ANK 4
FT REPEAT 64 115 ANK 4
FT REPEAT 116 146 ANK 4
FT REPEAT 147 281 ANK 4
FT REPEAT 282 214 ANK 4
FT REPEAT 215 243 ANK 4
FT REPEAT 244 280 ANK 4
FT REPEAT 281 310 ANK 4
FT REPEAT 311 340 ANK 4
FT REPEAT 341 379 ANK 13
FT REPEAT 380 412 ANK 13
FT REPEAT 413 446 ANK 13
FT REPEAT 447 480 ANK 13
SQ SEQUENCE 748 AA; 83609 MW; 29144.000000000000; 79.14.

Query Match
Best local similarity 29.1%; Score 43.5; DB 1; Length 766;
Matches 155; Conservative 97; Mismatches 161; Indels 14; Gaps 4;

QY 24 LLEKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 LLEKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 25 ASKEGHIVVEELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 ASKEGHIVVEELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 62 ASKSHASVSLDRAEVNCHQDQNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 ASKSHASVSLDRAEVNCHQDQNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 138 SVYPTTMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 SVYPTTMAKQRTQVVELLSHNPANFSTYSGY 137
QY 139 GRPTTMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 GRPTTMAKQRTQVVELLSHNPANFSTYSGY 137
QY 159 LAKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 LAKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 160 NHRDQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 NHRDQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 192 AMQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 AMQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 240 ENKSNLPGQVYDRAEVNCHQDQNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 ENKSNLPGQVYDRAEVNCHQDQNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 252 IVQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 IVQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 400 NARYVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 NARYVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 412 EKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 EKQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 420 WQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
D6 2 WQVDEBERNSGTPVLAELGVHIVKELKSGASLEHREKNTALMAKQRTQVVELLSHNPANFSTYSGY 137
QY 472 PLHVAIPRPSRRLAELL 348
D6 2 PLHVAIPRPSRRLAELL 348
QY 473 AVRAVAKGHSQIKLL 434
D6 2 AVRAVAKGHSQIKLL 434

RESULT 6
ID Y379 HUMAN STANDARD; PRT; 1559 AA.
AC Q15083;
DT 16-OCT-2001; Rel: 40, Created!
DI 16-OCT-2001; Rel: 40, Last sequence update!
DE 16-OCT-2001; Rel: 40, Last annotation update!
DE Hypothetical protein KIAA0379 (F14J08)
GN KIAA0379.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI:TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.

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TISSE=Brain;
MEDLINE=97349964; PubMed=9205841;
RA Nagase T., Ishikawa K., Nakatani D., Ohira M., Seki N.,
RA Miyajima N., Tanaka A., Kozani H., Nomura N., Ohara O.;
RT Prediction of the coding sequences of unidentified human genes. VII.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.
RD DNA Res. 4:141-150,1997.
CC 1. SIMILARITY: Contains at least 27 ANK repeats.
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CC or send an e-mail to: license@sib.ch.
DR EMBL: AB002377; SRA: CH33.2;
DR HSSP: P80144; 2MYV;
DR InterPro: IPR002110; ANK.
DR Pfam: PF00023; ank; 18.
DR PRINTS: PRO1415; ANKYRIN.
DR SMART: SMO0248; ANK REPEAT; 24.
DR PROSITE: PS00088; ANK REPEAT; 1.
DR PROSITE: PS00297; ANK REP REGION; 1.
KW Hypothetical protein; Repeat; ANK repeat.
FT NON TER 1
FT REPEAT 1 75 ANK 1
FT REPEAT 76 108 ANK 2
FT REPEAT 109 141 ANK 3
FT REPEAT 142 174 ANK 4
FT REPEAT 175 207 ANK 5
FT REPEAT 208 240 ANK 6
FT REPEAT 241 273 ANK 7
FT REPEAT 274 307 ANK 8
FT REPEAT 308 340 ANK 9
FT REPEAT 341 373 ANK 10
FT REPEAT 374 406 ANK 11
FT REPEAT 407 439 ANK 12
FT REPEAT 440 472 ANK 13
FT REPEAT 473 506 ANK 14
FT REPEAT 507 540 ANK 15
FT REPEAT 541 574 ANK 16
FT REPEAT 575 607 ANK 17
FT REPEAT 608 641 ANK 18
FT REPEAT 642 675 ANK 19
FT REPEAT 676 709 ANK 20
FT REPEAT 710 743 ANK 21
FT REPEAT 744 777 ANK 22
FT REPEAT 778 811 ANK 23
FT REPEAT 812 845 ANK 24
FT REPEAT 846 879 ANK 25
FT REPEAT 880 913 ANK 26
FT REPEAT 914 947 ANK 27
SQ SEQUENCE 1059 AA; 113465 MW; C1F55E6CFE494770 CRC64;

Query Match
Best local similarity 4.9%; Score 43.5; DB 1; Length 1059;
Matches 155; Conservative 96; Mismatches 239; Indels 127; Gaps 13;

QY 7 OSVINVEERITPALKALEKCKVDNERNEGCTPLMLAARQGVNVEIKELKNGANCNL 66
D6 20 QAIIFNGDPE ---VRAIIFKKEDINFDNKRTPPLHAAAYLGDAEIIELLSARVNA 75
QY 67 EDLDNR-----TALISASKEGHHIVVELKSGASLEHR----- 100
D6 76 KD-SKWLTP-LHRAVASCSEA---VQLLKHSADVARNDKWQTPPLHAAANKAVKCAE 130
QY 101 -----DMGWTALMAKQRTQVVELLSHNPANFSTYSGYVPTMAKGR 148
D6 131 ALVPLLSNWNVSCRAGRTAJHHAAFSGHGMVKLLSGANINAFD-KKDRRAIHAAAYM 189

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QY 149 CHADIVHLLQNGKVCNCKYCTTPHAAARSHLPCVHLLAGKANTGEGNSHTAL 238
 DQ 150 OSHTKVLVSHAEVTKCKKSKY:FLHAAASGMSVWVLLDGVWSPHVAHTH 249
 QY 209 TVAVKQYTCQVKFLK 234
 DQ 250 HVA YN QCVVHLLDGVWSPHVAHTH:FLHAAASGMSVWVLLDGVWSPHVAHTH 249
 QY 255 KUNTAHMAHSHHIEHVEHLLDGVWSPHVAHTH:FLHAAASGMSVWVLLDGVWSPHVAHTH 249
 DQ 256 256
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CY 107 SAYDKGDTTPJVAIRGRSRKRLAEIQRPHKO RLLYRPNKA RLTQYNL QIQKSLINQ 422
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CY 109 IFDAPHLATETDQMLGILYNSALAE ILSEITMATTIYATWYRYSRILNKSEF 424
DB 110 LRTQ----- 425
CY 111 EMRTFANQTEPLEFQSKLVLELT 426
DB 112 ----- 427
CY 113 IALISLSEADIVFRIVIVSIEEF RQWMAWALTRLAH WQWLLFATVPMVHRE 428
DB 114 VQVSSNNL 429
CY 115 EQTRAL----- 430
DB 116 PRSADQSTKATIQNAVINGVRFQWSESTREVEFTVY TAAKLTSTRVYVF 431
CY 117 TSLUAGREFG- PLATRIFFVETEEZ- CRRKMKETCH RQFVLAALVQGLIAJ 432
DB 118 SLEETVEIQNPVFWLSIKSNW LERHLAGSRK 433
CY 119 TLLAIFRVERPKHLYNAIL IALATVYLAFLVLR RTWQVQDSELSNAR 434
DB 120 VATHACIMVIFA LGRNLR 435
CY 121 ASKLKLRSEGF-----MKVLEEVFMAVYKTISETLQSLVTVIS LAGQFVYV 436
DB 122 SNKLEFVRSASSSKMKVLEHNL LTPSLVAVTIVTWE 437
CY 123 QMIVQVLFQSKPPFAL FASEE LIRNGDNLNNGSR LQNLH LQNLHLPV 438
DB 124 SLRPPRLNGQMSLQFVH VQCVNLSNFF 439
CY 125 LNSRGRNARKPKVTSNTNTHIYI TIRCKLIRFVZON L VQVLFALNKP 440
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CY 127 TRPRQMKTIKQNSFNTRKNTQWQWQ QUTINRQFQNSVTE LKQNSITPN 442
DB 128 RYVVEIQWVDSVVEELIQILANV LAKNSGPM 443
CY 129 W 963 444
DB 130 W 1117 445

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RESULT 8

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AC G95271 G95272 STANLARG 180
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DT 28-FEB-2003 (Ref. 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 4
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BA Ottenwelder B., Obermaier B., Vexes H.W., Gassenhuter J., W. -ann S.,
RL Submitted (JAN-2000) to the EMBL/GenBank/CDL databases.
CR EMBL: AL137551; CAB72807.1;
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 246 AA; 27255 MW; D1E19C628456EF2 CRC64;

Query March
Best Local Similarity 90.7%; Pred. No. 1, Gap 1;
Matches 205; Conservative 17; Mismatches 19; Indels 0; Gaps 37

QY 1463 LPSGSGESGTFVGTTPHCKMRIRERLEAKDGEVSPGUSAEITRTTAPFVTSAL 1522
DB 12 LKDCCKRAEYKRVAP... FSP EHSNADPTPLNAPN SGA 52

QY 1523 LKKRSSGVSRRSSPNLSNLSAATQQLKARLIELEHESGSPVQKRNLSHQD 1592
DB 53 LKKTSSSGVSRRSSPNLSNLSAATQQLKARLIELEHESGSPVQKRNLSHQD 112

QY 1583 P...A...MS...CSDEKKSPECSLSIASHRESKVAQKAYNLRTPSTVILNKAFTNPANT 1642
DB 113 P...A...MS...CSDEKKSPECSLSIASHRESKVAQKAYNLRTPSTVILNKAFTNPANT 172

QY 1643 NFEDEEGRETISOVILRPGSPSPNPAVKNELFENAKHESKRSSEYTRLSKASELH AAS 1703
DB 173 NFEDEEGRETISOVILRPGSPSPNPAVKNELFENAKHESKRSSEYTRLSKASELH AAS 232

QY 1702 SSTGFGERESIL 1715
DB 233 SSTGFGERESIL 246

RESULT 13
Q9H889 PRELIMINARY; PRT; 129 AA.
AC Q9H889;
DT 01-MAR-2001 (TRENDSrel. 16, Created)
DT 01-MAR-2001 (TRENDSrel. 16, Last sequence update)
DT 01-OCT-2002 (TRENDSrel. 22, Last annotation update)
DE Hypothetical protein FL13864
OS Homo sapiens (Human)
GC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
CX NCBI_TaxID:9606;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE:Thyroid;
RA Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
RA Tanase T., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
RA Arida N., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
RA Wakamatsu A., Nishikawa T., Nishikawa T., Nishikawa T., Nishikawa T.,
RT "NEO human cDNA sequencing project"
RL Submitted (AUG-2002) to the EMBL/GenBank/CDL databases.
CR EMBL: AK02926; BAB14728.1;
KW Hypothetical protein.
SQ SEQUENCE 129 AA; 14244 MW; 4B4F46513745B4 CRC64;

Query Match 6.8%; Score 599.5; ID 4; Length 129;
Best Local Similarity 90.7%; Pred. No. 4, Gap 1;
Matches 117; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 1598 MSICSEKKSPECSLSIASHRESKVAQKAYNLRTPSTVILNKAFTNPANTAPLAKQNGEIL 1647
DB 1 MSICSEKKSPECSLSIASHRESKVAQKAYNLRTPSTVILNKAFTNPANTAPLAKQNGEIL 60

QY 1648 EGIRRTSVILRPGSPSPNPAVKNELFENAKHESKRSSEYTRLSKASELH AASSESTG 1706
DB 61 EGIRRTSVILRPGSPSPNPAVKNELFENAKHESKRSSEYTRLSKASELH AASSESTG 129

QY 1707 FGERESIL 1715
DB 121 FGERESIL 129
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RESULT 11
Q8YT39 PRELIMINARY; PRT; 426 AA.
AC Q8YT39;
DT 01-MAR-2002 (TRENDSrel. 25, Created)
DT 01-MAR-2002 (TRENDSrel. 25, Last sequence update)
DT 01-MAR-2003 (TRENDSrel. 23, Last annotation update)
DE Hypothetical Protein AL12748;
CR AL12748;
OS Anabaena sp. (strain PCC 7120);
OC Bacacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc;
CX NCBI_TaxID:103693;
RN 1;
RP SEQUENCE FROM N.A.
RC MEDLINE:215952P5; PubMed:11759843;
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Triguichi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara Y., Matsuo M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimizu S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RL DNA Res. 8:205-215(2001);
CR EMBL: AP003590; BAB74447.1;
DE InterPro: IPR004110; ANK;
RPfam: PF00223; ANK; 12;
DR SMART: SM00248; ANK; 13;
DR PROSITE: PS0086; ANK REPEAT; 1;
DS PROSITE: PS0086; ANK REPEAT; 1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 426 AA; 43803 YW; CF03955043ACAA03 CRC64;
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Query Match 6.3%; Score 555; ID 16; Length 426;
Best Local Similarity 17.2%; Pred. No. 4, Gap 29;
Matches 149; Conservative 67; Mismatches 177; Indels 8; Gaps 6;

QY 8 VINVVEENIPAKALLEKQKVDPERNECSQTPUMJAAAGQNVVEIKELKNGANGNL-E 67
DB 9 LKVARSGI LKSGALLAAGVGVDICRDSGTTALMFAANLGYTEIVRSLLGGGANVNLAR 67

QY 65 QDNWNTALISASKEGHUHVVEELKSGASLEHRRMGNTALMWACYKGRDGVVLLLSHG 127
DB 68 KRYGLTALXLAASANOVDIVCLLSRGAHVATNEDGSTALMAAALKNVEVARVILLAAG 127

QY 128 AKPSVTGKQASVYFIWAAGRGHADIVHLLQNGAKVNCSDKYTTPLVWAARKHLECV 187
DB 128 ADVNITKQDILALKLAKRGGAAYVQLILPKNADANDEDEGETLLMLAARDGSGVY 186

QY 198 PHILAMKALVDEGANSNTALIVAKWRYTVSVKEILKRPKNVLTOKDGNALMIASKE 247
DB 187 QVLLAAGVINEQNGQSGTALLAAVAAAGNAGIAKILLDRGADVNHODDGSALJLATVE 246

QY 248 GHIEIVQDLIDAGTYVNIPIRSGDTVVGAVRGGHVEIVRALLQKYADIDIRGOD-NKTA 306
DB 247 GYVVVQVLLNCGANTGINKLQDTPILVAAALQHDQIVETLL-KYG-ANVHGQNLGETP 304

QY 307 LYWAVEKGLATMWRDILQCNPDTEICTKQGETPLIKATKRNIEVWELLDDKGAQSAVD 366
DB 305 LTLAASQGHATVRIILLOYGANAKIPASQDGTALIKATERNHPQVIGQLLAKGANVYQD 364

QY 367 KKGDTPLVVAIRSRRLAELLNPNKQGRLLLYRPNKAGET 407
DB 365 SVGTALIAAAGSYNKKVQILLEGADTNL---KRRGGYT 402
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RESULT 12
Q99407 PRELIMINARY; PRT; 1856 AA.
AC Q99407;
DT 01-MAY-1997 (TRENDSrel. 03, Created)
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DB 1588 PN2FGQD---HSDISS:RSPKPSLSGLPSSQNIHRTGPPVYACDTSLS 1644
CY 1618 KQTKV-----QAEVDAYREYIAAGCA KTNSTLS -- PESP HAYTIGUS 1665
LI 1645 KNDGSVTVTFADPLVDSEGLDQDQAEAC WAWVTFER QQAEPFATJRKVWS 1704
CY 1645 SSUGSHTLBOERKEGELQEDHRELKYS K VLDNSESJSTNEAN LSPITFEELE 1825
DB 1705 SE---CCEKKGSG 1724
CY 1826 KNDGSKLLPQKASRSPKIPOTAEAF RYVYAFDFERLESSTOPJTEHESKX 1885
DB 1905 K---SSEKSGS SEENPVEDLAMLDPG--BAE 1958
CY 1986 RTKPKAKQCTG--TQNHGATPFPFPPFEL LAGDPELHAWK 1996
DB 1999 ANSSLACWCHETSGSLESFAGAS 1999
CY 1999 ESSTPESJHHAAYDSLEKAGLDELEF LQEPF 1999
DB 1999 KTFANGHT--ASVLEKAPFETELQNTWQ FRELKPTCHLHLESPG 1964
CY 1987 EMSICSEKXSPSCS--LASSPHEKMACTPAYVHLSSTSTVTJNNVADLRKQNF 1644
DB 1986 -SPLTAYQSLERTSKAVIPKAPVAVLWVPEM 1999
CY 1645 DEIRG 1649
DB 1999 QREES 1995

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RESULT 14

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ID Q13769 PREXIMINAK; REF: 100 ZA
AC Q13769
DT 01-NOV-1996 (Treybirel, 01, Created)
DT 01-NOV-1996 (Treybirel, 01, Last annotated update)
DT 01-JUN-2002 (Treybirel, 21, Last annotated update)
DE Alt. unkyrin (variant 2,2).
CS Homo sapiens (human).
CC Eukaryota; Metazoa; Chordata; C1a 1a; Vertebrata; Primates; H1
CC Mammalia; Eutheria; Primates; C1a 1a; Hominidae; Homo
CC NCBI TaxID=9606;
LN 1
RP SEQUENCE FROM N.A.
RC Tissue:hematopoietic;
RX MEDLINE:9015410; PubMed=213119;
RA Lux S.E., Conn. K.W., Connor. V.
RT "Analysis of CD34, CD133, and CD133-related genes in human
RT structure with a family of 12 genes."
RT control structure.
RJ Nature 344:38-42, 1999.
DR EMBL: X16609; GenBank: U13111.
DR HSSP: Q08420; IAA:
DR InterPro: IPR02110; ANK.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000466; ZUS.
DR Pfam: PF00023; ank; 24.
DR Pfam: PF00511; death; 1.
DR Pfam: PF00791; ZUS; 1.
DR PRINTS: PR01415; ANKIRIN.
DR SMART: SM00248; ANK; 22.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00218; ZUS; 1.
DR PROSITE: PS00088; ANK_REPEAT; 20.
DR PROSITE: PS00297; ANK_REPEAT_REGION;
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
KW ANK repeat; Repeat.
SC SEQUENCE (219 AA; 14901; MW: 15440.9; pI: 5.04;

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Query Match 6.2%; Score 25; E-4; Length 119;
Pair Local Similarity 59.6%; Pref H 100;

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Matches 376; Conservative 270; Mismatches 604; Indels 574; Gaps 72;
CY 21 LKALLEKQDVERNEKQCTP:MLAAEQGNVEIKELLKNGANCNLED:DNWTLALISAK 80
DB 34 VRELYNGANYAOSQKQFTPLMAAQENHLEVVKELLNGANGVATEDGFTPLAVALQ 153
CY 81 RGE--- 81
DB 154 QRENVVAKLNYGTKGKVR:PALHIAARDQDTAAVLLQNDPNPDVLSKTGTPHIA 213
CY 84 -ITHVEELKSGASEHDMGSGWTALMAKYKGTUVVELLSHGKNSPTVGLQYS 199
DB 214 MYENINVAQLMARGANSTPQNGITNHAASRGNAV:VWLLLDGGAQTE-TKTQDE 272
CY 119 VPELIMAA-RUATVHLLNGLNJKVNSRYGTTPLVAAARKCHLECVNHLANGAOD 198
DB 274 QTPHCAAPYHVPISLLEDRAPQAKTKNLSPIHYAAGGDHLDVRLILQYDAED 112
CY 199 --- 199
DB 343 DITLDHGLTFAHLCHHRYAKV:LRKGFANSHALNGFTPTJHACKNHVWVWELLJK 192
CY 226 RNVNMLTQKNTALNKSGH:EIYVELLDAGTYVNPDRSGDTVLIGAVGGHVEI 285
DB 191 TQASIDAVTESHLTPRVASPMGHIPIVNLILQSGSPNSVNVKVEPLRVAAAGHTEV 452
CY 266 VVALQKYAGDIDRGDNKNTALYNAVEKGNATMYHCLLQCNPTCEICTKQGETPLKATK 345
DB 453 AKYLLONKRVNAKAKDQTPHICAAITGHINNMVALLENNANPNLATAGHTPHIAAR 512
CY 346 MRNIEVRLGLDKGAKSAVDKKGDTP:HVATIRSRSLAEILLNPKDGRLLVYRKNAG 405
DB 513 EGHVETVALLLEKESACQAKTKKQFTP:HVAAKYKGVAVALLER--PDA --HPNAG 566
CY 406 E TQYHLSHQ --- 406
DB 567 KAGDPLVAVYHNNLDVALLPESGSHSPANNCTPTCHIAAKQNCVAVARSILYGG 626
CY 428 ---HSPETDQMGVLYSALADLSEPTMOP-----PDC-- 462
DB 627 SANASVQ VITVHLAAGEHBNVALLSKQNGNJKSGLTPLHLVAGEHVPVADV 686
CY 463 ---AGLYAOKSOK SFLIKLEED-EMKTFACQCTEP:PFQFSWL 501
DB 687 LKKGWNTATPMGYTPHVAHVSHVGNLYKFKELHQADVNAKTKGY--SPCHAAQ 744
CY 502 ---VFTVITVGLGVAPVQ---TNIAIALSFLIALYIPFIVIFGGRSE 513
DB 740 HEDVAVGLGJ---ASPKWSSHTTTCIAAFEGYISVTEVILKVW --- 769
CY 554 KNNKAWDITAPAHVYHLLERKMPYNT:ELPQCTFALPVPFLPTQVAPLS-SVIGE 612
DB 790 TQSTFVLNLSAHR-MSFETVWVILDSLSLGEELS-----FKARRDSVDDEE 840
CY 613 TSLAEVATESHACTREFGFLATRIFR-----VFATTE-SQKKKKKTKTCLISFV 662
DB 841 KELLDEVPCHLWE -SPATPPIPCAMPETWIRSEEQEQASKEYQEDSLPS- 892
CY 663 LPLFVVLITAGITLALATFRTPKLTVNALISASVYGLAFVNCRTWQVLDLSLS 722
DB 891 ---SPATETSON--SPVASPVTFGLVSP-----MYDARSGS 925
CY 103 QRRRLERAAKHLKLESEFMKV:KCEVELKARMAKTIIDSTQNTQLVWITDGLDACEQ 782
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104 98 PLYMAGLNNHCTYKYLLENSANGQATATEDSTPLAVAGQGNORAVALLNDOTKGR 157
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127 585 ..... 22CAKWAQYFPIHVVVLL 123
128 594 EKHNSHVAJTLVWAAKRY 196

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Sequence 1

Sequence 1, Application US/0901485
 Patent No. 5824306

GENERAL INFORMATION:

APPLICANT: Tary, Liang
 APPLICANT: Bleck, E. Scott
 TITLE OF INVENTION: DIRECTORIALIA AND BENTON AVANTIN
 TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS, AND
 TITLE OF INVENTION: USES THEREOF
 NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Tary, Liang
 ADDRESSEE: Bleck, E. Scott
 STREET: 1825 Sharp Point Drive
 CITY: Fort Collins
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80525
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER US/0901485
FILING DATE:
CLASSIFICATION: 510
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/0901485
FILING DATE: 22 APR 1997
ATTORNEY/AGENT INFORMATION:
NAME: Tary, Liang
REGISTRATION NUMBER: 37,459
REFERENCE/DOC NO: 5824306
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970 494 1272
TELEFAX: 970 494 1272
INFORMATION FOR SEQUENCE:
SEQUENCE CHARACTERISTICS:
LENGTH: 1745 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-031-485-13

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Query Match 538; Score 466.5; DB 2; Length 1745;
Best local Similarity 20.4%; Pred. No. 1.2e 20;
Matches 158; Conservative 235; Mismatches 575; Indels 591; Gaps 73;
QY 14 EKHNSHVAJTLVWAAKRY 196
DB 267 KHAQAGVYHNSHVAJTLVWAAKRY 196
QY 72 ..... 22CAKWAQYFPIHVVVLL 123
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QY 392 ..... 22CAKWAQYFPIHVVVLL 123
DB 686 QEDVSVAAHNSHVAJTLVWAAKRY 196
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506 NAATRLTYTPHAAKEQOEVAALMLHSTOKTLLTKKGTFLHAAAYGNLPVAKSL 365
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351 WAAHLPKGAQVAVKKGITRLEDAFISPHLAELELLEN 391
624 IASTLHYKAKANAKKAGTPELACALRPPHMAAI IENINRQQAQAEHE IPMELCA 685
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686 QDRUVASABENFEAAIDKTRA VILHAYN 43
QINWVA 427
441 YLYANALADINENPTNQTLOV IYALWISJHFAKKEI EHEHETAGJOTELL 495
729 FLEHGRARVITPASVTP --- HANAOHONVVFILHIAHAYVHINHO 777
496 FQSKLIVETELLGAGALVFAH ICHHAAIALESPLALIVITFIVIVHHRHESW 555
778 --- TELSI 782
556 NWAAWALSTRARHIGYLLLEKLYKQVPHLEPHTKALGVRF --- LPTON 604
793 --- ABELGVSVVYALKKITHITVITVITVITTEERYIICUPZAVHETESD 530
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949 IITIRKAPOTPV --- YVHOKLARIHISSEHAI AS 986
733 KHKKKEGFPYKVLKCEVELMAVAFKUSHJACTAVIL --- IDAC 780
987 RILEXAPHAKFLOVILEPFAH --- FUREELVITRSLGQKARHQQEAT 1038
781 EOKVLUMG --- IVVLEHKEOPTAFASHHITIKALINQUNS 822
1039 EBAVOALVNESDAEELSCLONLHSTIRILHNFHM VFA --- VVHOPSEV 1090
423 VLEDSNIRHGYENIVHLPVUEHSENNASCHVTAALNITLITLILETTER 861
1091 VGFESQV ILSVYHPLA --- 1127
482 VSGQSLHNEKLSYALAGS --- 1127
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1349 RTHDRETAADGR --- IVEMAFPLAENQICP --- VTLATLPEYTS 1393
1111 PFQCVNPSOPHSYVSGLS --- QFJFFVYRAVPAVTSGLSS --- NT 1155
1394 PEP --- VWSKR --- IFYSEASLTXVYATHETALGCLPLARVALITLWHLAPALEV 1448

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DB 1487 SAL- QR:RDVVYREMOUPAEKLDGLBOTPVSHLSGPSITLSSTLLEVAGRRRHAETV 1444
QY 1260 TELS-SQPYTAN:SF --- EELHTAGLDE --- GAPHSNLSKQSQ 1297
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DB 1784 TGLSSGDAEIMTPTKEO 1722
RESULT 5
US-09-065-474-33
; Sequence 33, Application: US/07065474
; Patent No. 6863599
; GENERAL INFORMATION
; APPLICANT: Tang, Liang
; APPLICANT: Biehn, E. Scot
; TITLE OF INVENTION: LAROFILARIA AND BRUGIA ANKYRIN
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
; TITLE OF INVENTION: USES THEREOF
; NUMBER OF SEQUENCES: 171
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heskia Corporation
; STREET: 1925 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIA TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09065474
; FILING DATE: 24 APR 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: HW-5-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-065-474-33

Query Match 5.3%; Score 466.5; DB 3; Length 1745;
Best Local Similarity 20.4%; Pct. No. 1.2e-29;
Matches 358; Conservative 235; Mismatches 575; Indels 591; Gaps 71;

APPLICATION NUMBER: US/09/057,634
 FILING DATE: 21-Apr-2000
 CLASSIFICATION: <Unknown>
 EPIC APPLICATION DATA:
 APPLICATION NUMBER: 09/057,634
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Voisei, Paul Talkner, D
 REGISTRATION NUMBER: 37,453
 REFERENCE/DOCKET NUMBER: 4,503
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 970/493-1772
 TELEFAX: 970/494-9533
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1745 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Query March 5 38; Score: 466.3; E: 4e-104; Length: 1745;
 Best Local Similarity: 20.43; Pred. No. 1,000,000;
 Matches: 358; Complementarity: 237; Mismatches: 475; Indels: 197; Gaps: 733

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 DB 107 KKEIKNAATLLQHNNSQVTSKSHPTTHAKHKNENVACLEKFKGVNSVARNIS 246
 QY 72 W TALSSAKKEGHILVEKLEFASAK 97
 DB 279 PIRKATWERTNKVLLALJAVL KQPLLILHATASAKH KQVGLERKASAK 326
 QY 98 ERTVGVWALNW 110
 DB 327 TKTSLAPKVAAGVETVYVETPIVWAPVLSGVAFKIPKAGNKAFAKPTLH 366
 QY 111 ACKKRTIYVELLSHGANSVGHLYVTFELKALBPJHALLDGLKQKAPVNSQNY 370
 LF 167 ACKNSRTIKVELLSKTHAALFATREKSHPTKAMKMAINTVITVLCQANQVATY 441
 QY 171 GTTTLVWAKGHLKVKHLAGVWVTPQAGKALAVAVPTQVAFETKRSW 230
 LF 446 GSTPDLNANANTQIVRLVWVGAAGVAGARLLATLHLSAPKQTLVILLQANAGH 505
 QY 191 NUTEDRTAKVANKSGHFEVGLDGLAHTVETLKKVYVWVWVLEKTPQAL 590
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 QY 591 WELLSKAGKAVKQKHTPLKAKKQKSKKAKK 692
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 QY 592PKIRLLVPRKAKKHTVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 640
 LF 666 QERVSVAAEELVKNAAIDKKAQKHTLVWVWV 710
 QY 441 YELKSNALALKEPTKQPTQVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 475
 LF 728 FLHNGKAVSVITKASTPQAKALKQKQKAVKLEKKNHNTK 777
 QY 494 FQFSLVPLTLLQGLGLVAFKQKALALAKLSEALALVLEKLVKPRKESW 555
 LF 516 582
 QY 556 NWAKLSTRALHLYLELLEKMEKKELEKPLKAKVPRK 604
 LF 564AERLVSVVSEALKPTLLEKVLATITVLEKPTLQKQKALVWVWV 640

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 DB 1704 TGLSSGRADATWPTPTREK 1722

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: Windows 95
5  SOFTWARE: WCTPSP1-001 for Windows 95, Version 1.0
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US77/0-01,100
8  FILING DATE:
9  CLASSIFICATION:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US77/0-01,100
12 FILING DATE: 24-APR-1997
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Vetsco, Carol Talbot
15 REGISTRATION NUMBER: 47,413
16 REFERENCE/DOCKET NUMBER: BM-5
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: 970/493-7272
19 TELEFAX: 970/484-9500
20 INFORMATION FOR SEQ ID NO. 24
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 348 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: protein
26 PS-SC-C1: 483 28
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Search completed: November 21, 2003, 11:40:00
 Job time: 1:26 secs

CC specification.
 XX XX
 SC Sequence 1715 AA:
 Query Value 100.00, Score 8884, DB 22, Length 1715,
 Post-local Similarity 100.00, Pred. Number 0,
 Patches 1715, Conservative 0, Miscellaneous 0, Indels 0, Gaps 0.

QY 1 MSVLSLVYVYVEENIPALKALEKCKVDENNECQOTELMIAABQGNLEIVKELIKN 60
 DI 1 MSVLSLVYVYVEENIPALKALEKCKVDENNECQOTELMIAABQGNLEIVKELIKN 60
 QY 61 GANONLEILKWTALISASKEIRHVAVESLKKGVNLEHRDMGONTALMAKCYKGRDVV 120
 DI 61 GANONLEILKWTALISASKEIRHVAVESLKKGVNLEHRDMGONTALMAKCYKGRDVV 120
 QY 121 ELALSSEANFSTGTCYSVYPTIWAAGRHADIYHLLQNGAKVNCSDKYTTPLVWAAP 180
 DI 121 ELALSSEANFSTGTCYSVYPTIWAAGRHADIYHLLQNGAKVNCSDKYTTPLVWAAP 180
 QY 181 KHLKLVYHLGANGADVQEGANSVTALIVKGYTOSVKEILKRNPNVNLTKDQNTA 240
 DI 181 KHLKLVYHLGANGADVQEGANSVTALIVKGYTOSVKEILKRNPNVNLTKDQNTA 240
 QY 241 LMASKEHTEVQCLLDAGTVNIPDSRSETVAVGVRGGHVEIVRALCKYADIDRG 300
 DI 241 LMASKEHTEVQCLLDAGTVNIPDSRSETVAVGVRGGHVEIVRALCKYADIDRG 300
 QY 301 QOKKTALYMAVEKGNATWRCILOQNPTECTKQGETELIKATMRNIEVVELLSKGA 360
 DI 301 QOKKTALYMAVEKGNATWRCILOQNPTECTKQGETELIKATMRNIEVVELLSKGA 360
 QY 361 KVSAYDERDITLCHIAICBSPKCAFLILRNPKQGLLYRPNKACETPNIDCSHQSL 420
 DI 361 KVSAYDERDITLCHIAICBSPKCAFLILRNPKQGLLYRPNKACETPNIDCSHQSL 420
 QY 421 TQTCARRHSETTELHMLGLYVSSALADILSEPTMQPPICVGLYAKQSGKFLIKK 480
 DI 421 TQTCARRHSETTELHMLGLYVSSALADILSEPTMQPPICVGLYAKQSGKFLIKK 480
 QY 481 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 540
 DI 481 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 540
 QY 541 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 600
 DI 541 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 600
 QY 601 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 660
 DI 601 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 660
 QY 661 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 720
 DI 661 FTVIVPSESESMKAWVILSTRASHIYVLELLKMKLVNPPPELPSOTKALPVPELF 720
 QY 721 NSCRKPTIHAASKLRKSKSEGMKVLKGEVLMKAPKTIQSPCTONOTRWVITDGLDAC 780
 DI 721 NSCRKPTIHAASKLRKSKSEGMKVLKGEVLMKAPKTIQSPCTONOTRWVITDGLDAC 780
 QY 781 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 840
 DI 781 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 840
 QY 841 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 900
 DI 841 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 900
 QY 901 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 960
 DI 901 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 960
 QY 961 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 1020
 DI 961 EDEMKTFAQCTEPIECFSKIVSTILLVGLGLLPAFTVUPNKGIAVSFSLALIYF 1020

DB 181 KGRLECYKILLANGADVDGSGAKSMIALIVAVRHYTQSVFELIKENPKNVLTUWKLNTA 240
 QY 241 LMTASKESTEIVCDLLDASTVYVIFRPSDTLLGVAVKQDTEIVRAILLKYADILIPG 300
 DB 241 LMTASKESTEIVCDLLDASTVYVIFRPSDTLLGVAVKQDTEIVRAILLKYADILIPG 300
 QY 301 QNKTKALYAVKNGKATMVRDCLNDELEFETVDETELEVAPEMTEVYVILLKWA 360
 DB 301 QNKTKALYAVKNGKATMVRDCLNDELEFETVDETELEVAPEMTEVYVILLKWA 360
 QY 361 KVAVAKKQKTHITAIKPSSEFVAVKQDTEIVRAILLKYADILIPG 420
 DB 361 KVAVAKKQKTHITAIKPSSEFVAVKQDTEIVRAILLKYADILIPG 420
 QY 421 TQIFGAPHLSPTEIDGMLGVYVAVKQDTEIVRAILLKYADILIPG 480
 DB 421 TQIFGAPHLSPTEIDGMLGVYVAVKQDTEIVRAILLKYADILIPG 480
 QY 481 EDENKTFAGQOIEFLPOPSHLVIFTELEVAPEMTEVYVILLKWA 540
 DB 481 EDENKTFAGQOIEFLPOPSHLVIFTELEVAPEMTEVYVILLKWA 540
 QY 541 FVIVYQSGRFGESKNAWVSTRAHAYVIFTELEVAPEMTEVYVILLKWA 600
 DB 541 FVIVYQSGRFGESKNAWVSTRAHAYVIFTELEVAPEMTEVYVILLKWA 600
 QY 601 TDYNLSNVUGETSSAEMTATLQVDESEFETVDETELEVAPEMTEVYVILLKWA 660
 DB 601 TDYNLSNVUGETSSAEMTATLQVDESEFETVDETELEVAPEMTEVYVILLKWA 660
 QY 661 FVIFLEIFIKISGILLAIFFVQVDESEFETVDETELEVAPEMTEVYVILLKWA 720
 DB 661 FVIFLEIFIKISGILLAIFFVQVDESEFETVDETELEVAPEMTEVYVILLKWA 720
 QY 721 NSQPKLHRAASLHLKSKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 780
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 QY 781 EOLKVLNCTVAVFSKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 840
 DB 781 EOLKVLNCTVAVFSKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 840
 QY 841 LPVFKNSRLSNAPKFLVTSATVIFVQVDESEFETVDETELEVAPEMTEVYVILLKWA 900
 DB 841 LPVFKNSRLSNAPKFLVTSATVIFVQVDESEFETVDETELEVAPEMTEVYVILLKWA 900
 QY 901 KRTVRSKQVPTQKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 960
 DB 901 KRTVRSKQVPTQKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 960
 QY 961 FNMKPLASMINLEQWYFVAVKQDTEIVRAILLKYADILIPG 1020
 DB 961 FNMKPLASMINLEQWYFVAVKQDTEIVRAILLKYADILIPG 1020
 QY 1021 EIDGIRNEVFLSSRTPLVAVKQDTEIVRAILLKYADILIPG 1080
 DB 1021 EIDGIRNEVFLSSRTPLVAVKQDTEIVRAILLKYADILIPG 1080
 QY 1081 PPLPQEGPRAGSGVSGPSVAVKQDTEIVRAILLKYADILIPG 1140
 DB 1081 PPLPQEGPRAGSGVSGPSVAVKQDTEIVRAILLKYADILIPG 1140
 QY 1141 SGPARGVVLSNUNLVAVTEKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 1200
 DB 1141 SGPARGVVLSNUNLVAVTEKQKQVDESEFETVDETELEVAPEMTEVYVILLKWA 1200
 QY 1201 KEMKXNDHILFSTVLENKRAEETVDETELEVAPEMTEVYVILLKWA 1260
 DB 1201 KEMKXNDHILFSTVLENKRAEETVDETELEVAPEMTEVYVILLKWA 1260
 QY 1261 ELSQGTLYLNFSEELNTLQVDESEFETVDETELEVAPEMTEVYVILLKWA 1320
 DB 1261 ELSQGTLYLNFSEELNTLQVDESEFETVDETELEVAPEMTEVYVILLKWA 1320

QY 1321 DKYCAEYFAYREYIAQNSQLBGGPSTTISGRSSPHSTYYWQSSSGSIHNSLECEKG 1380
 DB 1321 DKYCAEYFAYREYIAQNSQLBGGPSTTISGRSSPHSTYYWQSSSGSIHNSLECEKG 1380
 QY 1381 KDSEPKATLAKKSGFLMFRSDVIDYSSSGVSTNDASPLDPTTEDEKSDQSGSKLLPGKKS 1440
 DB 1381 KDSEPKATLAKKSGFLMFRSDVIDYSSSGVSTNDASPLDPTTEDEKSDQSGSKLLPGKKS 1440
 QY 1441 SESSSFFQKAKKSGFLMFRSDVIDYSSSGVSTNDASPLDPTTEDEKSDQSGSKLLPGKKS 1500
 DB 1441 SESSSFFQKAKKSGFLMFRSDVIDYSSSGVSTNDASPLDPTTEDEKSDQSGSKLLPGKKS 1500
 QY 1501 ERSAEHTFELKAKYVSTALDKKQSSSGVSSSESSPHSLHNEVAICSEKXANLIE 1560
 DB 1501 ERSAEHTFELKAKYVSTALDKKQSSSGVSSSESSPHSLHNEVAICSEKXANLIE 1560
 QY 1561 LEQSHSGRFPDPSLSTGLQRTIARMSICSEDKKSPSECSLIASSPBNWPACOKAYN 1620
 DB 1561 LEQSHSGRFPDPSLSTGLQRTIARMSICSEDKKSPSECSLIASSPBNWPACOKAYN 1620
 QY 1621 NRPSTVYVNSAPANRANCNEVEGIRETSQVLRPSSSPNPTTIONENKSMTHKR 1680
 DB 1621 NRPSTVYVNSAPANRANCNEVEGIRETSQVLRPSSSPNPTTIONENKSMTHKR 1680
 QY 1681 SQSSYTRIKQPPPELHAAASSESTQFGEERESIL 1740
 DB 1681 SQSSYTRIKQPPPELHAAASSESTQFGEERESIL 1740
 RESULT 4
 AAC9694C
 ID AAC9694C standard; Protein: 1715 AA.
 XX
 AC AAC9694C;
 DT 30-JUL-2002 (first entry)
 XX Hu-AC Kidins220 (first entry)
 XX
 KW Kidins220; kinase D interacting substrate of 22kDa; cytosolic;
 KW neuroprotective; gene therapy; protein; kinase D; PKD; cancer;
 KW neurodegenerative disease; glioblastoma multiforme; prostate cancer;
 XX human.
 CS Human sapient.
 XX WK-91220396-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2401W-HRC3977.
 XX
 PS 06-SEP-2002; 26000N-B30449P.
 XX
 PA (INVER: IMPERIAL CANCER RES TECHNOLOGY LTD.
 XX
 PI Schiavo G, Iglesas T.
 XX
 DR WPI: 2002-31979/42.
 DR N-RSDH, ABK51220.
 XX
 PT Polypeptide kinase D interacting substrate of 220 kDa and
 PT polynucleotide, useful for identifying modulators useful in treating
 PT cancer and neurodegenerative diseases -
 XX
 PS Claim 33; Fig 11; 136pp; English.
 XX
 CC The invention relates to polypeptide comprising a kinase D interacting
 CC substrate of 220 kDa (Kidins220) from rat and human or their
 CC fragment, variant or fusion; provided that the protein is not the
 CC polypeptide encoded by Genbank Accession No. AB033076. Also included are
 CC a polynucleotide encoding Kidins220 provided that polynucleotide is

1621 MPHELSHLDPI:ARMSICSEKKEKSGSCSLASSPEENWPAQKAYNLHETSTVLNN 1650
 1632 NPAVAFVNFVNFEMEGIRHETSOVLHISSTNPTIOHNRKMTHKRQSSYTLISK 1691
 1681 NTATPAPNFVEIEGIRHETSOVLHISSTNPTIOHNRKMTHKRQSSYTLISK 1740
 1692 PFVEHRAASSTJGPEEFENL 1715
 1741 CASSEH AASSTJGPEEFENL 1715
 RASSTJG
 AAE25143
 AAE25143 standard; Protein; 1715 AA
 AAE25143;
 19-OCT-2002 (first entry)
 Rat ARMS protein.
 Ankyrin repeat-rich membrane spanning protein; ARMS; Neurotrophin
 ephrin; receptor tyrosine kinase; growth cone; neuronal; neuronal cell;
 diagnostic; imaging; rat.
 Rattus norvegicus.
 Key Location/Qualifiers
 Region 17-139
 Note "Ankyrin repeat"
 Region 154-143
 Note "N-terminal region"
 Domain 496-518
 Note "Transmembrane domain"
 Domain 525-546
 Note "Transmembrane domain"
 Region 573-615
 Note "Coop between TPL and CM3"
 Domain 661-640
 Note "Transmembrane domain"
 Domain 588-510
 Note "Transmembrane domain"
 Region 749-854
 Note "Carboxy tail"
 Region 840-1160
 Note "Carboxy tail"
 Region 1040-1033
 Note "Polybasic region"
 Domain 1011-1033
 Note "SAV domain"
 Binding site 1011-1033
 Note "PDZ binding site"
 WO200250273-A2
 27 JUN 2002.
 19-DEC-2001; 2001W-US48603.
 21-DEC-2000; 2000US-256909P.
 (UNYV : UNIV NEW YORK STATE.
 Chao MV, Kopp H;
 WPT; 2002-508800/54.
 N-PSDB; AAD41035.
 Isolated ankyrin repeat-rich membrane spanning ARMS polypeptide that
 is a target for phosphorylation by neurotrophin and ephrin receptor
 tyrosine kinases, useful as a marker for growth cones.
 Claim 1; Page 8; 94, 136pp; English.

The invention relates to ankyrin repeat-rich membrane spanning (ARMS)
 protein which is a down stream target of neurotrophin and ephrin
 receptor tyrosine kinases. ARMS DNA is useful for visualising the
 growth cone of neurons. ARMS protein is useful as an indicator of
 the biological activity of neurotrophins and ephrins, as a marker
 for neuronal cells which have the ability to undergo continued
 synaptic changes through adult life or for the presence and
 distribution of ARMS in such neuronal cells, or as a marker for
 growth cones. ARMS DNA is useful in diagnostic and imaging methods.
 The present sequence is rat ARMS protein.
 Sequence 1715 AA;
 Query Match 94.94; Score 8266; DB 2; Length 1715;
 Best Local Similarity 92.74; Pred. No. 0;
 Matches 1591; Conservative 53; Mismatches 70; Indels 2; Gaps 2.
 QY 1 YSVLSQVINYVEEENIPALKALEKCKVDPERNECCQTPLMIAAEGGNLEIVKELIKN 60
 DB 1 YSVLSQVINYVEEENIPALKALEKCKVDPERNECCQTPLMIAAEGGNLEIVKELIKN 60
 QY 61 GANCKLEMDKWTALISASKEGHVIVEELKCOVNLHHRDMGWTALMWACYKGRTOVV 120
 DB 61 GANCKLEMDKWTALISASKEGHVIVEELKCOVNLHHRDMGWTALMWACYKGRTOVV 120
 QY 121 ELLASHGAFNSVTGLQYSVYPIWAAGRGHADIVHLLONGAKYNCCKYGTTPVMAAR 180
 DB 121 ELLASHGAFNSVTGLQYSVYPIWAAGRGHADIVHLLONGAKYNCCKYGTTPVMAAR 180
 QY 181 KQLECVPHLLAMGADVDOEGANSNTALIVAVKGGYTQSVKEILKRNPNVNLTKDQNTA 240
 DB 181 KQLECVPHLLAMGADVDOEGANSNTALIVAVKGGYTQSVKEILKRNPNVNLTKDQNTA 240
 QY 241 LMIASKEHTIIVODILDACTYVNIPIRSGDTVLIGAVRGGHVIVALLQKYADIDIRG 300
 DB 241 LMIASKEHTIIVODILDACTYVNIPIRSGDTVLIGAVRGGHVIVALLQKYADIDIRG 300
 QY 301 CONKTALNVAVEKGNATWVRDILQCNPTTEICTKDGTEPLKATKMNIEVVELLCKGA 360
 DB 301 CONKTALNVAVEKGNATWVRDILQCNPTTEICTKDGTEPLKATKMNIEVVELLCKGA 360
 QY 361 KVSADKYGDTPLHIA:RGRSRKLAELLRNPKDORLIYRPNKAGETPYN:DCSHOKSIL 420
 DB 361 KVSADKYGDTPLHIA:RGRSRKLAELLRNPKDORLIYRPNKAGETPYN:DCSHOKSIL 420
 QY 421 TQIFENHLSPTIRHMLYLYLSAAGILSEFTWQPPICVGLYAKWGSKSFLLAKKL 480
 DB 421 TQIFENHLSPTIRHMLYLYLSAAGILSEFTWQPPICVGLYAKWGSKSFLLAKKL 480
 QY 481 EDEKTEAGGCIERLQPSW:VVELTLLGGGLLFAFTVHPNLGIASVLSHLALYIF 540
 DB 481 EDEKTEAGGCIERLQPSW:VVELTLLGGGLLFAFTVHPNLGIASVLSHLALYIF 540
 QY 541 FIVYFGHRRREGESNNWAWV:STELAPH:GYDELKLMFVNPPELPEQTTKALPVRF 600
 DB 541 FIVYFGHRRREGESNNWAWV:STELAPH:GYDELKLMFVNPPELPEQTTKALPVRF 600
 QY 601 TQYNPLSSVGGTSLAEMIATLSACEREFQFATLRFVFEKTEDTQCKKXKWKTCCLPS 660
 DB 601 TQYNPLSSVGGTSLAEMIATLSACEREFQFATLRFVFEKTEDTQCKKXKWKTCCLPS 660
 QY 661 FVIFLFT:SCIIISGITLLAIFRVDPKHTVNAVVISIASVGLAFVNCRTWQVLSLL 720
 DB 661 FVIFLFT:SCIIISGITLLAIFRVDPKHTVNAVVISIASVGLAFVNCRTWQVLSLL 720
 QY 721 NSQKRLHRAASKLHKASGEMKVLKCEVELMARMAKTIDSEFTQNTRLVVIIDGLDAC 780
 DB 721 NSQKRLHRAASKLHKASGEMKVLKCEVELMARMAKTIDSEFTQNTRLVVIIDGLDAC 780
 QY 781 ECKKVLQVLTVRVLESKGFIA:PASDPH:IKAINCNLSVLSDNSINGHDYWRN:VH 840
 DB 781 ECKKVLQVLTVRVLESKGFIA:PASDPH:IKAINCNLSVLSDNSINGHDYWRN:VH 840

[illegible][illegible]

[illegible]

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KW      Hypoetical protein: AKK repeat, Repeat.
SQ      SEQUENCE 1026 AA: 188239 MW: 430.46867E00RICA CRC64:

Query Match          5.9%: Score 502.5; DB 11; Length 1036;
Residual Similarity 19.8%: Pred No. 5.1e-25;
Matches 406; Conservative 246; Mismatches 612; Indels 793; Gaps 82;

14  EEKATIAKALLERKKVDYDERNECQOTPEUMIAAEQGNLEIVKELINGANGANCHEEDNWT 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
56  KESPEVTEVTELLQREANVDAAATKKGTATLHIAASAGCAEVVYVLTNGAVVAQSQNGFT 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
74  ALISNPVDPHIVTELLKCYNLSHRHKGWGTALMMWACYKGTGDVWELL 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136  PLYMAQPSHLEEVAFELLNGASQATGEGTPEVALQOQHDQVSSLEENDTKGKVR 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
125  -----SHGAMPSV*GL----- 135
186  LPAHIAAGNEDTKGAALLNDNTVADVESKSGFTPLHIAAHYGNINVTALLNRAAAVD 245
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
136  ---QVSVPVTKAAGRGHACIVHLLIQKAKVNCSDKYGTTPVMAARKG----- 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
246  FTAHWVTPHVASRGNWVKLLDQKAKIDAKTRDGLTEHCGARSCHFCVWVEWLLD 305
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183  -----HLECVKHLAMGADVDQEGANSMTALIVVVKGYGYS 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304  PSAPIQSTFKSLSPQKATQDHLNCCVLLQINVFVDVNTCYLTAFVAHCHGHYKV 365
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
220  VKEHLKPLPNTCTKQGNALMASKE----- 247
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
366  AKVILKQASNAKALNGFTPLHIAAKNR:RYMELLKHGASIQNVTSSTLPIHYAIF 425
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
148  TCHTEIVTLLDASTVYKIPDSSTVTLTGAVRGGVEIVRALLQKYADIDINGQNKTA 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
426  MSHVNVGIMENHSPNTNVSGETALHMAARSGQAEVVRVLDVQGAQVEAKAKDQTP 485
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
307  LYKAVLPGRHWKILQNPETHCTKQGETPLKATKRNIEVWELLQKJAKYSAMD 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
486  LKISAFLEARTVQCLQOGASPMATSGYTTFLHLMAREGHEQVAFLDHTASLIT 545
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
367  KQJLPLDLAGRGRKLAELLENKQGLLYRENKAGETPNIDCSHGKSLTQLEGA 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
546  KQSPTEVMAKYKLEVASLQKAS-----PDAAQ-----KSLTTPHYA 589
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
427  PHLSTELQVQWELKSSA:ADTISFTMOPPIQVGIYAQSGSKSFLLKLEDEMKT 486
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
443  AH-----KQHYVA-----LLDQASPHAAV----- 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
487  PHALQLKQPSNLYPLTMDQGRKELPAPTHFNPLGIANLSFLALLPFFIVIP 546
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
514  -----NATPLHIAAKKNCMIATSL-----DEY 536
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
547  QG-----HRESHWKAVLSTPLARHICVLLKLYFNVPPELPCTTKAIPVRFLPT 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
537  GDAKAVLQ-----IASVHLAQSHQDVQVLSLSN-----A 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
602  DYVRLSLHETSLAEVHATISDACEHEFGFIATPLRFYKTE-----DTQKKKW 652
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
612  KVNLSNGULTEL-----HLAAQERVYVAEVLVNOGAHVCAQTKQY 614
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613  KKCQNLHVPFLFTIGCIISSITLLAFRVPQKILTVNAVILSIASVYGLAFVLCRTW 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
715  -----THIV-----GCHYGNIKI-----VNFLLQHSKAV-----NAKT- 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
711  KOVLSLNSQKELHNAASKLHLKSEFPMVKCEVELMARMAKTIDSTFNQTPLVV 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
744  -----KNGTALHCAQAQQGTHIINV-----LQONASPNELTVNGTALAI 795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
771  LKQKTAELKRVLCLETVRVDFSGKPTIAFASDPHIIKALQNLKASVLPSDNLNQH 832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
846  -----LWLVVTLKVFTEHNTTITTEKKM-----NYPETMEVILMSDGEF 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
847  QVWVLLQVQDNGASKEVATNGVWPSQSTTIGCEDADRPNVLSLGEN----- 892
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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420 TQIFAPHLSPEDTDCQXGNYLAKAGACQLSEPTVQPIVAGVAGWAGSKSELEKFL 479
481 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 540
489 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 539
541 EVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 600
540 FVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 599
601 TYNALVAGWGLTCLAVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 660
610 TYNALVAGWGLTCLAVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 659
620 TYNALVAGWGLTCLAVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 720
660 FVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 719
721 NSQKELVNAASKLHKLKQFJEMFQF EVELVAKMARTLSEPTQNGTQVWVLDGJLAC 780
720 NSQKELVNAASKLHKLKQFJEMFQF EVELVAKMARTLSEPTQNGTQVWVLDGJLAC 779
781 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 840
780 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 839
841 LPVFNKSGLSNARKLVLVNAQNGWVNOTTNGCEDAPRVSQNSLAVTGLSKTAN 900
840 LPVFNKSGLSNARKLVLVNAQNGWVNOTTNGCEDAPRVSQNSLAVTGLSKTAN 899
901 RSTYPRRCQWRTITRQKARLITRQKARLITRQKARLITRQKARLITRQKARLIT 960
900 RSTYPRRCQWRTITRQKARLITRQKARLITRQKARLITRQKARLITRQKARLIT 959
961 FVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 1020
960 FVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 1019
1021 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1080
1020 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1079
1081 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1140
1080 EBNKTFACQCIETFCFQWLVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1139
1140 FVIVYFGRBEGESNNWAWVTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANFSE 1199
1144 APQWVNLNLSNVCANVCEKQFTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANF 1203
1200 APQWVNLNLSNVCANVCEKQFTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANF 1259
1204 NMVFEKHLPRSTVLEKRLVAVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1263
1240 NMVFEKHLPRSTVLEKRLVAVVITLQCGGRLPAPTHVPHGLGVANFSEALNLEF 1319
1264 SQTPYTLNFSFEELNTGLNLEKQFTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANF 1323
1320 SQTPYTLNFSFEELNTGLNLEKQFTEFACQWLVVITLQCGGRLPAPTHVPHGLGVANF 1379
1324 QAEVVDAYRYIAQXSCLEGGSTTQAEVVDAYRYIAQXSCLEGGSTTQAEVVDAYRYIA 1383
1380 QAEVVDAYRYIAQXSCLEGGSTTQAEVVDAYRYIAQXSCLEGGSTTQAEVVDAYRYIA 1439
1384 EPKPDQKQKFLMKRGVIVVNSGVSJYVTDQASTDPITEDEKSKSGSKSLPKKASSER 1443
1440 EPKPDQKQKFLMKRGVIVVNSGVSJYVTDQASTDPITEDEKSKSGSKSLPKKASSER 1499
1444 SSJFQDQKQKFLMKRGVIVVNSGVSJYVTDQASTDPITEDEKSKSGSKSLPKKASSER 1503

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1500 SSJFQDQKQKFLMKRGVIVVNSGVSJYVTDQASTDPITEDEKSKSGSKSLPKKASSER 1559
1534 AEPTEFTTAKREVSDALMLKKKSSDCGVSSSESSPNHSEHNEVADDSQLEKAKLIELE 1563
1560 AEPTEFTTAKREVSDALMLKKKSSDCGVSSSESSPNHSEHNEVADDSQLEKAKLIELE 1619
1564 DSHSKKEFHHSJHGLADPTLAKMSLSEKSKKSESECSLASSPEENWAPACQKAYNLRT 1623
1560 DSHSKKEFHHSJHGLADPTLAKMSLSEKSKKSESECSLASSPEENWAPACQKAYNLRT 1679
1564 RSTVNLNNSAPANRANCTEMESIRETSQVLPSSSPNPTTIQENILKSYTHKRSQ 1683
1580 RSTVNLNNSAPANRANCTEMESIRETSQVLPSSSPNPTTIQENILKSYTHKRSQ 1739
1684 SSYTKLSKQFTELHAAASSSTGFESEPSIL 1715
1740 SSYTKLSKQFTELHAAASSSTGFESEPSIL 1771

RESULT 5
US-10-117-229-7
; Sequence 7, Application US/10:17229
; Publication No. US2003:09625A1
; GENERAL INFORMATION
; APPLICANT: Origene Technologies, Inc.
; TITLE OF INVENTION: Human Kid:ns220pc
; FILE REFERENCE: 90104 R1
; CURRENT APPLICATION NUMBER: US/10:117,229
; CURRENT FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 7
; LENGTH: 1762
; TYPE: PNT
; ORGANISM: Rattus norvegicus
US-10-117-229-7

Query Match 94.1% Score 8362.5; DB 12; Length 1762;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 1616; Conservative 47; Mismatches 50; Indels 51; Gaps 4;

QY 1 XSVLLSGVINYVEENIPALKAILEKQKQVDEENECQCTPKMAEQQNLEIVKELKN 40
DB 1 XSVLLSGVINYVEENIPALKAILEKQKQVDEENECQCTPKMAEQQNLEIVKELKN 60
QY 61 XSVLLSGVINYVEENIPALKAILEKQKQVDEENECQCTPKMAEQQNLEIVKELKN 100
DB 61 XSVLLSGVINYVEENIPALKAILEKQKQVDEENECQCTPKMAEQQNLEIVKELKN 120
QY 121 ELLLSRDPSPVTGLQYSVPIIWAAGRGHADIHVEELKSGASLEHRONGWTALMWACYKPTDV 180
DB 121 ELLLSRDPSPVTGLQYSVPIIWAAGRGHADIHVEELKSGASLEHRONGWTALMWACYKPTDV 179
QY 181 KQLEKVPYHLLAMGADVQEGANSKATLIVAKGYGTYOSVKEILKRNPNVNLTDKGNTA 240
DB 181 KQLEKVPYHLLAMGADVQEGANSKATLIVAKGYGTYOSVKEILKRNPNVNLTDKGNTA 239
QY 241 LMIASFEHIEIVQCLLDAGTVNIPDRSGDTVLIGAVRGGHVEIVRALQKYADIDIRG 300
DB 241 LMIASFEHIEIVQCLLDAGTVNIPDRSGDTVLIGAVRGGHVEIVRALQKYADIDIRG 299
QY 301 QDNKTALVWAVEKGNATWVRDILQCNPTETCTKDGETPLIKATMRNIEVVELLQKGA 360
DB 301 QDNKTALVWAVEKGNATWVRDILQCNPTETCTKDGETPLIKATMRNIEVVELLQKGA 359
QY 361 KVSAYCKKQVPLHVAIRGRSRKLAELLRNPKQGRLLYRNKAGETPNYINDCSHQKSL 420
DB 361 KVSAYCKKQVPLHVAIRGRSRKLAELLRNPKQGRLLYRNKAGETPNYINDCSHQKSL 419
QY 421 TQIFAPHLSPEDTDCQXGNYLAKAGACQLSEPTVQPIVAGVAGWAGSKSELEKFL 480
DB 421 TQIFAPHLSPEDTDCQXGNYLAKAGACQLSEPTVQPIVAGVAGWAGSKSELEKFL 479

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541 FIVVYFOORCESSWMAWASTELARHIELELELEMEVHELELETKALPKELE 640
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QY 1690 RSORNYNENIKRPFELHAAASSSTCHGEPRESIL 1715
 DB 1691 RSORNYNENIKRPFELHAAASSSTCHGEPRESIL 1715

RESULT B
 US 10 117 129-3
 Sequence 3, Appl 3, US 10 117 129-3
 Publication No 3, US 10 117 129-3
 GENERAL INFORMATION
 APPLICANT: GRIGORIY KONSTANTINOVICH, IND
 TITLE OF INVENT: N-Substituted 2,3-Di-
 FILE REFERENCE: 99 174 R1
 CURRENT APPLICATION NUMBER: US/10/117,129
 CURRENT FILING DATE: 2003-04-08
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: Patent in version 3.0
 SEQ ID NO 3
 LENGTH: 1184
 TYPE: PRT
 ORGANISM: Homo sapiens
 US 10 117 129-3

Query Match: 64.4%, Score 449.5, DB 12, Length 1184
 Best Local Similarity: 99.3%, Pred. No: 0
 Matches 1184, Conservative 0, Mismatches 0, Indels 1, Gaps 1

QY 1 MSVLLSGQVNVVERENIPALKALEKKDYDERNECCQTPMTAAAGQNELEVKELIKN 60
 DB 1 MSVLLSGQVNVVERENIPALKALEKKDYDERNECCQTPMTAAAGQNELEVKELIKN 60
 QY 61 GANCLF LQMTALSSASKEHIVIVELELKQVNLERHDMGGWTALYACYKRTDWW 120
 DB 61 GANCLF LQMTALSSASKEHIVIVELELKQVNLERHDMGGWTALYACYKRTDWW 120
 QY 121 ELKMRHNSLNTLYLSVFIWAAGRHADIVLELLONGAKVNCSSKYCTPLVWAAAR 180
 DB 121 ELKMRHNSLNTLYLSVFIWAAGRHADIVLELLONGAKVNCSSKYCTPLVWAAAR 180
 QY 122 ELKMRHNSLNTLYLSVFIWAAGRHADIVLELLONGAKVNCSSKYCTPLVWAAAR 179
 DB 122 ELKMRHNSLNTLYLSVFIWAAGRHADIVLELLONGAKVNCSSKYCTPLVWAAAR 179
 QY 161 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 240
 DB 161 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 240
 QY 180 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 239
 DB 180 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 239
 QY 181 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 181 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 182 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 182 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 183 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 183 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 184 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 184 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 185 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 185 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 186 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 186 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 187 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 187 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 188 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 188 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 189 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 189 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 190 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
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 DB 191 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 192 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 192 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 193 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 193 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
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 DB 194 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
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 DB 195 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
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 DB 196 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 197 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 197 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 198 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 198 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
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 DB 199 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 QY 200 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180
 DB 200 KGHCPVYKELAMRVDEGNANSTALTVAKGYGTQSVKEILRNPNVNLTKDGNAT 180


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PRIORITY FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO: 6338
LENGTH: 705
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: MISC FEATURE
LOCATION: (344)
NAME/KEY: MISC FEATURE
LOCATION: (344)
OTHER INFORMATION: Xaa equals any of the 20 naturally occurring amino acids
LOCATION: (337)
OTHER INFORMATION: Xaa equals any of the 20 naturally occurring amino acids
US 10-104 598 6174

Query Match          34 35      Score 100.0%, DB 100 Length 705
Best Local Similarity 98.5%      Evid. No. 120 204 Gaps 17
Matches 587 Conservative 21 Mismatches 47 Indels 17 Gaps 17

CY 62 AKNLEKQKNTALISA FEHVLIVETDPTVLEHSHDPAKAWAYEAFRTGVE 121
DB 26 SKNLEKLVNTALLSAWE QVHIVETDPTVLEHSHDPAKAWAYEAFRTGVE 57
CY 122 LLLSHGAPSVTGLQSVTPTLWAPG HSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 181
DB 89 LLLSHGAPSVTGL QSVYPTLWAGHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 146
CY 182 GHLECVKHLAAGAWTJGAGASNTALIVAVP QVLECVKHLAAGAWTJGAGASNTAL 241
DB 147 GHLECVKHLAAGAWT JGAGASNTALIVAVP QVLECVKHLAAGAWTJGAGASNTAL 204
CY 242 MAAKSGHTEIVQLLDAHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 301
DB 207 MAAKSGHTEIVQLLDAHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 266
CY 302 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 341
DB 267 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 299
CY 362 VVAVDEKGTPTJHATF INDFPLAHSILQSF QSVYPTLWAGHSHGIVETDPTVLEHSHDPAK 421
DB 329 VVAVDEKGTPTJHATF INDFPLAHSILQSF QSVYPTLWAGHSHGIVETDPTVLEHSHDPAK 384
CY 422 QTF KASH QTFKASH QTFKASH QTFKASH QTFKASH QTFKASH QTFKASH 481
DB 384 QTF KASH QTFKASH QTFKASH QTFKASH QTFKASH QTFKASH QTFKASH 440
CY 482 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 541
DB 447 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 400
CY 542 IVIVYVGRSGESKNNAWVLTSTLAPHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 601
DB 507 IVIVYVGRSGESKNNAWVLTSTLAPHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 560
CY 602 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 661
DB 567 DSKALYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 520

RESULT 11
US-09 835 789A-17
Sequence 17, Application US/00-03789A
Patent No. US20020377458A1
GENERAL INFORMATION
APPLICANT: Ni et al.
TITLE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, Polypeptides, and
FILE OF INVENTION: Antibodies
FILE REFERENCE: PTO1491
CURRENT APPLICATION NUMBER: US/00-03789A
CURRENT FILING DATE: 2001-04-17
PRIORITY FILING DATE: 1999-11-17
PRIORITY APPLICATION NUMBER: PCT/US00/08466

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PRIORITY FILING DATE: 2002-10-17
PRIORITY APPLICATION NUMBER: 467/59,585
PRIORITY FILING DATE: 1999-10-18
PRIORITY APPLICATION NUMBER: 60/167,246
PRIORITY FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO: 17
LENGTH: 551
TYPE: PRT
ORGANISM: Homo sapiens
US-09 835 789A-17

Query Match          32 33      Score 98.1%, DB 99 Length 551
Best Local Similarity 99.8%      Evid. No. 120 192
Matches 550 Conservative 0 Mismatches 2 Indels 17 Gaps 17

CY 102 MGONTALWACYSKRTDWWVELLSHGANPSVTGLQSVYPTLWAGHSHGIVETDPTVLEHSHDPAK 161
DB 1 MGONTALWACYSKRTDWWVELLSHGANPSVTGL QSVYPTLWAGHSHGIVETDPTVLEHSHDPAK 59
CY 162 AKVNCHEIVETPTLVAAAKKHLECVKHLAAGAWTJGAGASNTALIVAVP QVLECVKHLAAGAWT 221
DB 60 AKVNCHEIVETPTLVAAAKKHLECVKHLAAGAWTJGAGASNTALIVAVP QVLECVKHLAAGAWT 119
CY 222 ESKKRNHNVLTETKQONTALMIASKEGHFEYVQCLLDAGTYVN: PDRSDTVLIGAVRG 281
DB 120 ESKKRNHNVLTETKQONTALMIASKEGHFEYVQCLLDAGTYVN: PDRSDTVLIGAVRG 179
CY 282 HVEIV-KAL QYAL QDIRQENKTAIYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 341
DB 180 HVEIV-KAL QYAL QDIRQENKTAIYMAVEKGNATMVRD LQCCNPOTETCTKOGETPL 299
CY 342 KATKPNHNVVELLSHGANPSVTGLQSVYPTLWAGHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 401
DB 340 KATKPNHNVVELLSHGANPSVTGLQSVYPTLWAGHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 299
CY 402 NKAGETTYNDGSHOKSILQTFGASHHSPITQSCMLGYDLYSSALADILSEPTMQPPI 461
DB 300 NKAGETTYNDGSHOKSILQTFGASHHSPITQSCMLGYDLYSSALADILSEPTMQPPI 359
CY 462 QVQVLAAGSGSHLKKLEDEMKTFAHQDQEPILQFQSNLIVETLILCGGILGILFAFTV 521
DB 400 QVQVLAAGSGSHLKKLEDEMKTFAHQDQEPILQFQSNLIVETLILCGGILGILFAFTV 419
CY 522 HSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 581
DB 479 HSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 479
CY 582 NPEELHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 641
DB 480 NPEELHSHGIVETDPTVLEHSHDPAKAWAYEAFRTGVE 479
CY 642 KTDQ LQFQKX 653
DB 640 KTDQ LQFQKX 551

RESULT 12
US 10-175 042-17
Sequence 17, Application US/10175042
Patent No. US2003018170A1
GENERAL INFORMATION
APPLICANT: Ni et al.
TITLE OF INVENTION: Death Domain-Containing Receptor Polynucleotides, and
FILE OF INVENTION: Antibodies
FILE REFERENCE: PTO1491
CURRENT APPLICATION NUMBER: US/10-175,042
CURRENT FILING DATE: 2003-06-20
PRIORITY FILING DATE: 2001-04-17
PRIORITY APPLICATION NUMBER: PCT/US00/08466

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167 ACCKNRKIKVIELIKYKAAHEAT TESRLTJAAVAFMGALIVIVYK. JAAQAVATV 445
171 GTTPAAVAAKSGHLECVKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
446 GEITPAAVAAKSGHLECVKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
231 KTEKQKNTALIAKAEHTEITVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
506 NAATRLTYTHAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
291 QYVACDIFQKNTALIAKAEHTEITVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
566 ERGTNDIEGQKNTALIAKAEHTEITVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
351 VVELLCKKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
626 IASTLHYKANAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
392 -----PKGRLLVYKNTALIAKAEHTEITVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
686 QRRVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
441 YNYSALADILSEFPCIPVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
728 FLIENGARVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
501 LIVETLILGQKNTALIAKAEHTEITVYKLLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
761 -----YVLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
561 ESTLAAHLYLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
782 -----YVLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
410 GUTLAAHLYLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
834 ESENGITAAHLYLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
661 -----YVLEKAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
894 QRRVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
682 KVTALVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
954 KVTALVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
738 KVTALVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
992 AFVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
796 LQMLVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1943 QVLLVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
829 NISCHVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1096 QVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
887 LQVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1116 QVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
942 RLAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1191 LLSKQVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
972 LTBQVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1251 EATAVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1326 LQVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236
1309 GRVAAVAGVJGMAASYTALIVAKVINTVSCALIKENH 236

1065 DVRAAEFATISRLAYPPLHRECFAPSGYSPSPVSCSTSENGPACGVSPQPHSS 1124
1359 DGR-----VVEKEKRAENLPCTP-----VCTLAILPBYTS-----PEMVVS 1399
1359 --YYSWTPQGHFYNPQSPAPAP-VLLNS:NVDAVCEKLL-----C 1165
1488 KKQVYSEASTKRYVAGAPHEAEPKINLFARVALLIGADWHLAPALEVTDIDIRQVHHQ 1459
1156 IESLQDQALPJCYTITKAN:N-GRVLAQCCHDEKKEMNN-----F 1202
1458 LVGLAVTLPINTIKKQATPVALBSALQIRGDCDVREMDRAEKLDGLGTPVSHIS 1519
1528 QMILPRTVEM--RNAE--SRVPEDERFLESSESG-PAPHGEPARASHNEL 1257
1528 GPSITLSITLEVAGURRRAEVMAOQRLAQEPFFQGVNGTGPCPEPKESFHEE 1579
1254 PHTLSSQTPYILNPSFEELNTLGLSGAPHSKLSQCSQTRTPSLSS:NSQSS:ES 1317
1580 EVAVS-----EIRTVYKTE-RHVHDSSENGPIVEERTITTYEDOVAVNEE 1624
1316 KUTOKVQAEYRCAVREYVLAQSGPSTTISGRSSPHSTYMGSSSSQGS 1370
1678 EVDKIVLHNSSEKMDRVREVEVAFQOE-----TSKEGTSCQTTHEKEKQDQGS 1679
1371 IESNLEKESKSETPK-CGSEKSELMKRGDVIDYSSGVSTNDASP-LDPTTEED 1424
1680 LKTVYKSHVRCIFFDQGETS-----ANETGLSSDAITMTPTTKED 1722

RESULT 5
US-09-065 474-33
Sequence 33, Application US/09065474
Patent No 6063599
GENERAL INFORMATION:
APPLICANT: Targis, Brian
APPLICANT: Blum, E. Scot
TITLE OF INVENTION: DROPHILARIA AND BRUGIA ARKYRIN
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Targis, Brian, Ph.D.
ADDRESS: Targis Corporation
STREET: 1820 East Point Drive
CITY: Point Point
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Microsoft for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,474
FILING DATE: 24 APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Verger, Carol Takington
REGISTRATION NUMBER: 37,455
REFERENCE/DOCKET NUMBER: HW-5-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/491-7272
TELEFAX: 970/494-9505
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1745 amino acids
TYPE: amino acid
TOPOLAGY: linear
MOLECULE TYPE: linear
US-09-065 474-33


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Patent No. 6225786
GENERAL INFORMATION:
APPLICANT: Motorola, Inc.
TITLE OF INVENTION: NO. 6225786
FILE REFERENCE: 44574-5002
CURRENT APPLICATION NUMBER: 44574-5002
EARLIER FILING DATE: 1997-03-01
EARLIER APPLICATION NUMBER: 44574-5002
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent Ver. 2.0
SEQ ID NO: 2
LENGTH: 1386
TYPE: PRT
ORGANISM: Homo sapiens
US-09-052 259.2

Query Match 4 93 30.00 100 100 100 100 100 100 100
Best Local Similarity 30.53, Percent 100, 100 100 100 100 100 100 100 100
Matches 120; Conservative 100; Mismatches 100; Indels 100; Gaps 100

CY 14 EREHFAKALKER...
DE 30 KANFKWELLKUGAS...
CY 74 ALIASK...
DE 90 ALHVAAS...
CY 113 T...
DE 110 T...
CY 123 W...
DE 129 K...
CY 251 V...
DE 266 A...
CY 313 K...
DE 318 E...
CY 373 A...
DE 388 J...
CY 410 A...
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Best Local Similarity 22.03; Percent 100, 100 100 100 100 100 100 100 100 100
Matches 225; Conservative 149; Mismatches 118; Indels 100; Gaps 100

CY 5 ISQSV...
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DE 196 R...
CY 123 L...
DE 456 T...
CY 183 H...
DE 516 Y...
CY 243 L...
DE 543 L...
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RESULT 12

US-09-392-812A-4

Sequence 4, Application US/09/42812A

Patent No. 6537778

GENERAL INFORMATION:

APPLICANT: Zuker, Charles S

APPLICANT: Walker, Richard G

APPLICANT: Wallingford, Aaron

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: A Eukaryotic Model for the Transcriptional Control

FILE REFERENCE: 22307E-09700US

CURRENT APPLICATION NUMBER: US/09/42812A

CURRENT FILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 4

LENGTH: 1619

TYPE: PRT

ORGANISM: Drosophila melanogaster

FEATURE:

OTHER INFORMATION: amino acid sequence derived from cDNA

OTHER INFORMATION: sequence

US-09-392-812A-4

Query Match

Best Local Similarity 25.18; Score 4.28; DB 4; Length 1619

Matches 136; Conservative 97; Mismatches 222; Indels 1; Gaps 18;

CY 29 KQVNERECQTPPLIAAGQTNILVPELIRYANVLEHLEKWTALISA-KCHGVHVE 88

DB 651 KAMFQSSVQWTPPLIAAHEHREHVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 710

CY 89 ELLKQVHLEHREHREHREHREHREHREHREHREHREHREHREHREHREHREH 147

DB 711 ALLTKAFINASKSVGTALIAAVVPHVVEHLEKWTALISAAPVDVQETE PSMALIAV 769

CY 148 RGHADIVLEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 207

DB 770 SGQVEVQCLLELGANIVDALELLELLELLELLELLELLELLELLELLELLELLE 796

CY 208 LIVAVQGYTQSVREILKRNKRN VQVTFQDNALM-ASKSEHREHVEHLEKWTALISA 264

DB 799 VAAQNYSEVAKGLEIQDQSHVLAHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 856

CY 265 IPDSNPQVNLIAVPHREHREHREHREHREHREHREHREHREHREHREHREHREH 910

DB 857 ARRTFQATQCLIAVPHREHREHREHREHREHREHREHREHREHREHREHREHREH 918

CY 301 QCRK TATYWAEEQV 349

DB 917 STNLRINSKKGLITPLVAAYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 974

CY 318 TPLIAKMRNIEVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 395

DB 977 TELAAAFSGNRYVRLKNSGVVLAATLEHVEHLEKWTALISAAPVDVQETE PSMALIAV 1034

CY 396 RLIVPFGAGTPPNIDCSHQSKLITLP KSHLSSTEDQVEMLGHVHREHREHREHREH 449

DB 1035 ELQSCQENGRTGTHIAAMPHIQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1590

CY 450 ---DIIESEPTMQPPI---CVGSAVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 501

DB 1091 EWWKLICAGASPRSENYKAAIKVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1150

CY 502 IV 503

DB 1151 VV 1152

RESULT 13

US-09 031-485-26

Sequence 28, Application US/09031485

Patent No. 5824356

GENERAL INFORMATION:

APPLICANT: Tang, Liang

APPLICANT: Blum, E. Scott

TITLE OF INVENTION: DROSOPHILARIA AND BRUGIA ANKYRIN

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND

TITLE OF INVENTION: USES THEREOF

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkingdon Vetter, Ph.D.

ADDRESSEE: Hesk Corporation

STREET: 1825 Shoup Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/031,485

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/847,423

FILING DATE: 24 APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Vetter, Carol Talkingdon

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: HW-5

TELECOMMUNICATIONS INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/494-9525

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US 09-031-485-28

Query Match 4.28; Score 144; DB 2; Length 348;

Best Local Similarity 33.78; P-Val 7e-24;

Matches 177; Conservative 48; Mismatches 144; Indels 18; Gaps 4;

CY 45 ASQSHREHVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 164

DB 44 AARAGHLEHVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 163

CY 105 KVALMAVYKGTQVVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 164

DB 104 NTAHIAHAGELIVTLVENGANVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 162

CY 165 KNSDYKVTPLVAARKGHLEHVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 224

DB 163 ALSTEVEHLEKWTALISAAPVDVQETE PSMALIAVREGNIVHVS 218

CY 225 KNPVNLTDKQNTALMTASKEHREHVEHLEKWTALISAAPVDVQETE PSMALIAV 284

DB 219 QNEHNSDVSKSGEPLHIAAHYGNVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 278

CY 285 IVRALQKQVADIQDQCKNTALYWAKEGNATMVRDILQCNPDTEICTKGETPLIKAT 344

DB 279 KVSLLIANSVVIDCR-----TRDLL-----TPDKCAS 305

CY 345 KKNIEVWELLDRGAKVSAVDKGDTPHIA 376

DB 304 RSGHDVWVQV 337

RESULT 14

US-08-847 4,24A-28

```

1 Patent No. 6063597
2 GENERAL INFORMATION:
3 APPLICANT: Taro, Utsugi
4 APPLICANT: Biogen, E. Saito
5 TITLE OF INVENTION: DIFELAFILAN AND PROSTA ANKYRIN
6 TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
7 TITLE OF INVENTION: DNA SEQUENCE
8 NUMBER OF SEQUENCES: 171
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Taro Takamizawa, Ph.D.
11 ADDRESSEE: Biogen Corporation
12 STREET: 1825 Shattuck Drive
13 CITY: Fort Collins
14 STATE: Colorado
15 COUNTRY: USA
16 ZIP: 80525
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: Windows 95
21 SOFTWARE: Aldrich/Intel for Windows, Version 7.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/065,474
24 FILING DATE: 24 Apr. 1998
25 CLASSIFICATION:
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Verstep, Carol Takamizawa
28 REGISTRATION NUMBER: 37,459
29 REFERENCE/DOCKET NUMBER: HW 5 01
30 TELECOMMUNICATIONS INFORMATION:
31 TELEPHONE: 970/493 7072
32 TELEFAX: 970/494 1505
33 INFORMATION FOR SEQ ID NO. 28
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 348 amino acids
36 TYPE: amino acid
37 TOPMOLOGY: linear
38 MOLECULE TYPE: protein
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Revised: November 21, 2003, 14:48:59

Accession: GBR118737; OMV142306

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankryrin; ankryrin repeat homology

Keywords: alternative splicing

F:2-1856/Product: ankryrin 1; erythrocyte form; seratus predicted; KAT

F:2-1513/Product: ankryrin 2; erythrocyte form; us predicted; KAT

F:44-76/Domain: ankryrin repeat homology; AN1

F:77-109/Domain: ankryrin repeat homology; AN2

F:110-143/Domain: ankryrin repeat homology; AN3

F:143-171/Domain: ankryrin repeat homology; AN4

F:172-204/Domain: ankryrin repeat homology; AN5

F:235-237/Domain: ankryrin repeat homology; AN6

F:238-270/Domain: ankryrin repeat homology; AN7

F:272-303/Domain: ankryrin repeat homology; AN8

F:324-336/Domain: ankryrin repeat homology; AN9

F:337-369/Domain: ankryrin repeat homology; AN10

F:370-402/Domain: ankryrin repeat homology; AN11

F:433-435/Domain: ankryrin repeat homology; AN12

F:436-468/Domain: ankryrin repeat homology; AN13

F:469-501/Domain: ankryrin repeat homology; AN14

F:502-534/Domain: ankryrin repeat homology; AN15

F:535-567/Domain: ankryrin repeat homology; AN16

F:568-600/Domain: ankryrin repeat homology; AN17

F:601-633/Domain: ankryrin repeat homology; AN18

F:634-666/Domain: ankryrin repeat homology; AN19

F:667-699/Domain: ankryrin repeat homology; AN20

F:732-732/Domain: ankryrin repeat homology; AN21

F:733-765/Domain: ankryrin repeat homology; AN22

F:766-798/Domain: ankryrin repeat homology; AN23

Query Match

Best local similarity 19.61; Score 18.47; E-value 1e-47

Matches 373; Conservative 247; Moderate 459; Simple 147; Inf. 72

QY 21 LKALERKFWDERKEDACTYV LKALQNTVRELEKRNKQ NLEDLNTELEKASR 40

DB 32 LKALERKFWDERKEDACTYV LKALQNTVRELEKRNKQ NLEDLNTELEKASR 40

DB 94 VPELVYGVANVAGSQGPTVYVAGVNHILVAVPELENMAGLVATELEPTCAVALQ 183

QY 81 ERMVIVRELEKQV KQENRQVWIAVVA 111

DB 154 QURENVAILNYTKGVPLDILKASNNITETRAVLQNTNPPVLSLPTPLHIA 213

QY 112 CYKQRTVVEVLLSHGASNV QLY 139

DB 214 AIVENLAKALLERQSSWPTVYVAGVNHILVAVPELENMAGLVATELEPTCAVALQ 183

QY 140 YPLIAGVRELEKQV KQENRQVWIAVVA 111

DB 274 TRLVAVRSHVRELEKQV KQENRQVWIAVVA 111

QY 199 KQENRQVWIAVVA 111

DB 334 TRLVAVRSHVRELEKQV KQENRQVWIAVVA 111

QY 227 NPNVNTKQNTALNTASKSRRIVVAVLQNTNPPVLSLPTPLHIA 213

DB 394 GASIDAVTESGLTPIHVASERREIVVAVLQNTNPPVLSLPTPLHIA 213

QY 287 RALLAKVADIDRGCKNTALNTASKSRRIVVAVLQNTNPPVLSLPTPLHIA 213

DB 454 KYLLQKAVNNAKEDCTPCHCAVALQNTNPPVLSLPTPLHIA 213

QY 347 RNVIEVELLDGAKVSAVCKKQVPIHIAIPVKKIAELITPREKQETVPRKAGE 406

DB 514 GIVEIVALLERKASQCKTKGPTELHVAALAKVPAVELLE RDA HPSNACK 567

QY 407 -TPYKIDCSHQKSLTQTFSAHLSHTETDQNGYDLYSSALADILSFTNQPIV 462

DB 568 NGLTIVAVAVHNNLDVALLPFLVSHSRAVNI QIPIHIAKQV QEVA 618

QY 463 VGLYAKVSGKFLKKLEDEKPTALQIETVPSNLTIVELIDQV LKALFA 518

DB 619 RELVAVLSANAEV QVTH LKALFA 518

QY 519 PTVHPNGLAVASLFIADLYIFFEIVYFGRRREGESKNWAVLSTRLAPHIOYLELLK 577

DB 657 KQANGVAKSHSLTPELV ADEG HVPVADVLEK 690

QY 578 --- LKPVNPELPEQTTKALVPRFDF TQYNPLSSVG -GETSLA 616

DB 591 GVMVCNTRENGVTPHVASHYGNLKVFLHQADVNAKTKLGVSPILHQAACQGHIVV 750

QY 617 EMI ATLSDAKESRFGELA-TRLPVRPKTECTQKKKKKTKCLIPSV 662

DB 751 TLLLRNAGSRNEVSSDQTPALAKELGVISVTDVLKVW-TDET SPV 796

QY 663 LPUFLILVHSHTLALFVAPKHL TVNAVLAISIASVVG LAFVLNCRWMC 714

DB 797 J VSDKHMSPPETVDEIL-DVSEDEGEELISFAER 832

QY 715 VADSLNKRKRJHNAASKHKLKSGHMKVLCVELMARMAKTIDSTFOTNQLVVI 774

DB 933 --DSPVVEFEKELDFVPLQDVVSPAIPR-PC AMPETVVRSEDEQASKEY 884

QY 775 DGLDAREQVQVIONLSTVAVLS- KGFIAIAPADP HIILK 814

DB 885 DESLINSPPATETSDNISPVASPVETGLVFPYVDARQSGMRSGHNLGVIPPTCA 944

QY 615 ALNGLNLSVLRDSNINGHDYRN-IVHLPVEL-NSRGLS 851

DB 945 APTREITKLVAKCKLSTPEPLASEECLASRIALGPTGAQFLSPVIVEIPHASCHRG 1002

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DB 1206 NV TAVPYKAFV 1243

QY 1114 GGVAHQVHSSVYSMTGPCHPPYKNGNAPAPV VLNSLNVDAVE K 1062

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DB 1282 SRDIEVLEGNLS FALSG NLVPVKAQAQOPSPHOSFRENLAM 1325

QY 1223 AESHVVEPPEPFLSESSSGPAHGFEPARASHNE LPHTELS 1263

DB 1326 PVKVPDSSREPQSGSLSEKAKYVEDTCHILCHLN:TMPCKAGSGAEDRR 1376

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DB 1377 RTPTPALRYLSILSES:PGSLSGTEQAEKMAV:SEHLGLSWAELARELCQFSVEDIN 1433

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DB 1434 RIRVENPNSLLEQSVALLNLWVIREG QNANMENLYALQSD 1474

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 QY 813 QVNTVNLVHLVNLSPKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 810
 DE 812 QVAKASAPKLSQGEVYQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 809
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 S37771
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 Cloned: Mus musculus (house mouse)
 CDate: 27-May-1994 sequence revision 31 Aug-1995 #text_change 13 Aug-1999
 CAccession: S37771
 Ribiker-Weber, C.S.; Walter, R.A.; Peters, L.J.; Hall, E.J.; Lux, S.E.; Barker, J.E.
 C.Biol. Chem. 268, 4511-4540, 1993
 ATitle: Complex patterns of sequence variation and multiple 5' and 3' ends are found
 AReference number: S37771; MIMD:91252835; PMID:8486643
 AAccession: S37771
 AStatus: preliminary
 A.Molecule type: mRNA
 A.Positives: 1:1845, 1:1846, 1:1847
 A.Cross-references: EMBL:X69043; MIMD:911816; PIDN:CAA48801.1; PID:911817
 C.Sequence: ankyrin, ankyrin repeat homology
 C.Keywords: alternative splicing
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 Matches 178; Conservative 284; Mismatches 653; Gaps 57.

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 DE 98 VRELVNYANVAQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 157
 QY 81 QGVHVEVLEKQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 111
 DE 158 QGHENVAHLNVGQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 217
 QY 112 QV 119
 DE 218 QV 277
 QY 140 YPLVAAWQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 198
 DE 178 TPCHAAWQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 177

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DE 864 TSDSLIPSPATETSDNISPSASH... ..L... ..L... ..L... 943
QY 815 --- ... ..L... ..L... ..L... 951
DE 944 APRITPTVVKQK... ..L... ..L... ..L... 1021
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DT 01-APR 1993 (Rev. 25, Created:
DT 01-OCT 1996 (Rev. 34, Last sequence update:
DT 24-FEB 2003 (Rev. 41, Last annotation update:
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CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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RX MEDLINE=93102465; PubMed=1930053;
RA Outo E., Kuntze M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114 (41-253):1991;
RN 12;
RP REVISIONS;
RA Carpenter S.;
RL Submitted (MAY 1993) to the EMBL/GenBank/CCDS databases.
PN 1;
RP SEQUENCE FROM N.A. (ISOPROX 1);
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Cran W., Kordeli E., Bennett V.;
RT "443 kD ankyrinB: structure of the major developmentally regulated
RT domain and subcellular localization in myelinated axons.";
RL J. Cell Biol. 133 (43):473:1993;
RN 13;
RP SEQUENCE FROM 461-5 FROM N.A.
RX MEDLINE=9209911; PubMed=1111057;
RA Tan W., Kottmann J.C., Yang Feng T., Francke U., Sahr K.E.,
RA Lux S.E., Ward M., Forget P.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
RT ankyrin gene.";
RL Genomics 10:856-864(1991);
CC -- FUNCTION: Attach integral membrane proteins to cytoskeletal
CC elements. Also bind to cytoskeletal proteins.
CC -- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId:Q01484 1; Sequence=Displayed;
CC Name=2;
CC IsoId:Q01484 2; Sequence=VSP_000267, VSP_000268;
CC Name=3;
CC IsoId:Q01484 3; Sequence=VSP_000268;
CC -- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN
CC -- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -- SIMILARITY: Contains 21 ANK repeats.
CC -- SIMILARITY: Contains 1 death domain.

```


DB	620	QOASRPAAGANGYTPHIAAKKXNVOHATILLYGADANAVTSQJASVHLASJEBVDF	679
QY	439	LOVELYSSACADILSEPTVOP	466
DB	680	VSLILUNANVNLNSKSHLTPHIALEPUNAPVUNQANVACTWYVILVATH	619
QY	467	ADQOSUK-SPLK KLEENKFTALVHP	419
DB	740	VNIRKIVELJOSAFVAKTPIVTHQAAQ	495
QY	520	TORPY	469
DB	784	NASINELTQNTAGSARLGLVNLVPL	434
QY	670	GYLELAKVFNVPPEL	616
DB	835	NVPTKMEVMSQCEVKKANEH	984
QY	617	EMIALSLANCEREGFACR	666
DB	895	GPCLEKGCOSLAPAGYHSC	940
QY	487	YICSTISGILLATPRCP	417
DB	941	LVR-KSHLTFREDSQELKVAWALTELLILVSSFTLHLSQVAF	994
QY	718	SILDSKRPVHNAKSLFKSKHJVC	773
DB	994	OSMKOSPHG	1029
QY	774	LDGLDAGC-KVACMLTVFVLE	813
DB	1016	KPHKLAN	1055
QY	844	YMRH-1VHVLVFNKSLMAREP	892
DB	1056	EDRVIVELTHFOSVRG	1102
QY	894	L-GRKALSRDTPVPRV	950
DB	1133	LINVGBELISPELOKRRVPLIF	1150
QY	761	BELLERAN	1005
DB	1151	SHILHETVLDQASPEKATP	1196
QY	1006	LRDQ-TPFVLEH	1045
DB	1197	AT	1221
QY	1066	VFAKRLSTLGLAYDUTLH	1124
DB	1284	PPINSETHQKAGS	1354
QY	1124	SYSLVPSQPPFNRSQFAPHVLL	1173
DB	1288	ADQPHITGT	1301
QY	1174	LFOCTTKKANKINQV	1220
DB	1302	YRHLQVYKAKVVFANKNUP	1352
QY	1221	KNAHSVVPFDPRLSSSSQFALHARA	1269
DB	1353	RSKITEVDEKPIVV-SYGNLADTP	1411
QY	1270	LNPSFRLNTGLDEGAPHSUMK	1329
DB	1412	USFLNKRTKGQVQVAVENINILVHKKRKA	1463
QY	1310	AYRE	1376

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1464 ALPKRVSSTPFGWIKSFGAT-----RS:RP YTYSYKPFPSRPYQSWTAPITV-----1511
1377 QEKXGSHKPTDGRKSFIMKRGCVLDYSSGVSTNCASPLQPI-----TEEDSKSQCSS-1432
1514 -----PQPAKSGF-----TSLSSSSSNTFSAPLKSIMSVSPSP:KSTLGAS 1556
1433 KLLPGKSHRSPLFDLKLKGSRLP-----YOKLPSEDESGT-----BESNTP:-----1480
1557 TSSVPSLAKVASPDS-IRYSSSMIKTYVSSPYNIOVSSGTLARAFAPATFATPLKGLA 1615
1481 -----LEFKGSKAKQYVER VFKSPE-----HSAEP:RTFI KAKYV:SDAL 1621
1516 SNTSPSSSSSTPTASSLERS:ITNFIASPKSNIMYSSSLLPKKS:ITSAPLSSP: 1675
1522 -----IRKUSDSGVSSSELSPPKSA:ANEVA-----QDSQLEKAN---LIE-- 1560
1476 KSVVSHVFPVQVWISSAKITVASSLSRSPKQPGHAEVALVNGS:SPILKYVSSSTLNGT 1735
1541 -LEFPHLSGKPGIPHSLSGLQLPITARKS:GSEDKKSPSECSLIASSSELENW7ACQ 1615
1736 KATATLQHS:SSATNSVSVSSVMATETVEKVSFTTAYFPSP:RP SYVSAAP----- 1786
1616 KAYNLSRSTVTNNKSNAPARANKCNFJENEGIRTSQVILLRPS-- PNPPT:CN 1670
1787 SAPQSRTKASALYV:SLSSISAT:--SVTSSITVTVSVVNV:HPALKK: 1819
1421 ENLKSMTFSSQSS- YTRLSKDPPELHAASS 1702
1640 POSNSTTAAAL-SPIKLTITETHCPHF:SKTS 1873

RESULT 5
YB23 ERYAN
ID YB24 HUXAN S ACHWC; PRT: 768 AA.
AC QULJ7;
CT 16 OCT-2001 (Rel 45, Created)
CT 16 OCT-2001 (Rel 45, Last sequence update)
CT 28 FEB-2003 (Rel 41, Last annotation update)
DE Hypothetical protein KIAA1223 (Fragment)
GN KIAA1223
OS Homo sapiens (90.4%)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM NIA
SC Tissue Panel
EX MIM:602094; PubMed:44620
RA Miller J, Bhatia A, Li J, Kienker S, Hironaka M, Komura N
RA 1
RI A collection of overlapping sequences of unidentified human genes. XV.
RI The complete sequences of 160 new cDNA clones from brain which code
RI for large proteins in vitro.
RL DNA seq 6137-61 1999.
CC -- SIMILARITY: Clones at least 14 ANK repeats.
CC
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CC or send an email to license@isb-sit.ch).
CC
CC EX01: AR33049; KIAA6537;
CC HSP; P42771; ID:
CC IntActPro: IPRO02117; ANK.
CC Pfam: PF00023; ank_14.
CC PRINTS: PR01415; ANKPRIN.
CC SMART: SM00248; ANK_13.
CC PROSITE: PSS0244; ANK_REPEAT; 13.
CC PROSITE: PSS0249; ANK_REPEAT_REGION; 1.
CC Hypothetical protein ERYAN; ANK repeat.
CC
CC DR DR033049; KIAA6537;
CC HSP; P42771; ID:
CC IntActPro: IPRO02117; ANK.
CC Pfam: PF00023; ank_14.
CC PRINTS: PR01415; ANKPRIN.
CC SMART: SM00248; ANK_13.
CC PROSITE: PSS0244; ANK_REPEAT; 13.
CC PROSITE: PSS0249; ANK_REPEAT_REGION; 1.
CC Hypothetical protein ERYAN; ANK repeat.
CC

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